#### **SEARCH REQUEST FORM**

#### Scientific and Technical Information Center

Requester's Full Name:		Examiner # :	Date:
Art Unit:	Phone Number 30	Serial Number:	
Mail Box and Bldg/Roc	om Location:	Results Format Preferred (circ	ele): PAPER DISK E-MAIL
	ch is submitted, please *******	prioritize searches in order of	need. :**********
Include the elected species outility of the invention. Defi	r structures, keywords, synony	describe as specifically as possible the ons, acronyms, and registry numbers, as special meaning. Give examples or releasins, and abstract.	nd combine with the concept or
Title of Invention:			
	Date:		
*For Sequence Searches Only appropriate serial number.	* Please include all pertinent info	ormation (parent, child, divisional, or issue	ed patent numbers) along with the

Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov

STAFF USE ONLY Type of Search Vendors and cost where applicable NA Sequence (#) STN\_\_\_ Dialog Searcher Phone #: Searcher Location: Questel/Orbit Structure (#) Bibliographic Dr.Link Lexis/Nexis\_\_\_\_\_ Litigation Searcher Prep & Review Time: Fulltext Sequence Systems ... 6,3 WWW/Internet \_\_\_\_ Clerical Prep Time: Patent Family 10 Other (specify)



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Title:
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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### ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX259747	RESULT 1
Lorenz,M., Kriz,R., Weich,N. and Shaw,G.D. A p-selectin glycoprotein ligand (psgl-1) binding protein and uses therefor	Bukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae; Homo. 1	Homo sapiens	human.		AX259747 1 GI:16508826	AX259747	Sequence 1 from Patent WO0173028.	AX259747 951 bp DNA linear PAT 26-0CT-2001		

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Location/Qualifiers
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/db_xref="G:16508827"
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/translation="MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLD
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Fondation Jean Dausset-Ceph (FR)
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Mammalia, Eutheria; Frimates; Catarrhini; Hominidae; Homo
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/translation="HSSRTPGHTQPWFLEPWSMASPEHPGSPGCMGPITGCTARTQGE
APATGEDLEMPGPDGHLDTHSGLSSNSSMTTRELQQXWQNQXCRWKHVKLLFEIASAR
IEERKVSKFVVVQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIEDVEFPR
FHLTGHPAEMICEPRPALQEVLGLLYAIPTVPPSFFFIDFILFPAFAGERRLQRLQ
YPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHEDFPAFAFAAGERRLQRLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6 from Patent WO0172822.
                                                                                                                                                                                                                                                        Hugot, J.P., Thomas, G., Zouali, M., Lesage, S. and Chamaillard Genes involved in intestinal inflammatory diseases and use Patent: Wo 0173822-A f 04-007-2001, Fondation Jean Dausset-Ceph (FR)
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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5426. .5577
                                                  7273.
                                                                                                               /db_xref="taxon:9606"
1. 161
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                                                                                                         AUTHORS
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Local Similarity 100.0%, Fred. No. 5.1e-82;
hes 670; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGCTCCGGAGGCCCACGCCCCGAGGCATCACCCTGAAGGAGCTCACTGTGGGAGAATA
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                              1 (bases 1 to 163319)
Hugot, J.P., Chamaillard, M., Zouali, H., Lesage, S., Cozard, J.!
Belaiche, J., Almer, S., Tysk, C., O'Morain, C.A., Gassull, M.,
Binder, V., Finkel, Y., Cortot, A., Modigliani, R., Laurent-Puic
Gower-Rousseau, C., Macry, J., Colombel, J.F., Sahbatou, M. and
Thomas, G.
                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                         HSA303140 163319 bp INA linear Homo sapiens NOD2 gene for LRR-containing protein, AJ303140 GI.14488148 LRR-containing protein; NOD2 gene.
                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
susceptibility to Crohn's disease
               Association of NOD2 leucine-rich repeat
                                                                                                                                                                                               human
                                                                                                                                                        Metazoa;
                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                variants
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                                                                 Laurent-Puig, P.
                                                                                                     Cezard, J.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
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ATVEANGLAAFLLOHVGELPVENMLDFLEAATCKKYMAKLTTVVSAGSRFLSTYDGAET
LCLEDIYTENVLEVWADVGMAGSPGKSPATLGLEELFSTFGHLNDDADTVLLVGEAGS
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RKVVTSRPAAVSAFLRKYIRTEENLKGFSEQGIFELVLKFHRFGYNADFLIFFLLGETS
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SEGKDSSVAALLQKAEPHNLQITAAFAGFLKSLSHEHWGLLAGCGTSEKALLRRQACABW
CLARSLPYHFHSLFPAPAFCKSYHAMPGFTNLIRSLYEMQCEPLAPFAFFTNVHL
KLTFCSVGPTECAALAFVLQHLRRPVALQLDYNSVGDIGVEQLLPCLGVCKALYLRON
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NISDRGICKLIECCHLREDOLKALFNNKLTDGCAHSMAKLACRQNFLANFLONG
NISDRGICKLIECCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLREDOLCHLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="LRR-containing protein"
/protein_id="CAC42117.1"
/protein_id="CAC42117.1"
/db_xref_"GI.14488149"
/translation="MCSQEAPQAQRSQLVELLVSGSLEGFESVLDWLLSWEVLSWEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(98448 98905,106807 106912,109510 1113;
115517 115600,115821 115904,118855 118938,
121552 121635,1222370 1122313,124418 124501,
128745 128828,130674 130746)
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115517 115600, J15821 115904, J18455 118438,
121552 121635, J22230 122313, J24418 124501,
124524 128828, J10674 131094)
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/db_xref="taxon:9606"
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Query Match 70.5%; Score 670; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 2.7e-82;
Matches 670; Conservative 0; Mismatches 0;
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                                               72940 ACGGCGCTATTCCGACTTCGCGAAGCTCCAGAAAGCGCTGCTGAAGAAGACGTTCAGGGAGGA 7288
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                                                                                                                                                                                                     Submitted (11-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mirchell Prive, Walnut Creek, CA 34538, USA On Jan 11, 2002 this sequence version replaced gi:18057072. Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
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Alamos, NM 87545, USA
3 (bases 1 to 16973)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Submitted (20-MAY-1999) Center for Human Genome Studies,
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POE Joint Genome Institute.
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DOE Joint Genome Institute.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero.
                                                                                                                       1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
                                                                                                          of this entry's ASN.1 file.
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AF395844 942 bp
Mus musculus SNX20 (Snx20) mRNA,
AF395844
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Best Local Similarity
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                                                                                              CCASCTCCT93AF95CCCACSCCCCT3A95CATCATCTT3AA93A3CTCACTTST5CCACAAAAA 28299
                                                                                                                           CCAGCTCCGGAGGCCCAGGCCCCGAGGCAGTGAAGGAAGCTCACTGTGCGAGAATA
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CCTGCACTGA 38309
                                                 CCTGCACTGA 951
                                                                                                                                                                                                                                               CCGCCTGGCCTACGCGCTGGGCAAGGACTTCGTGACTCTGCAGGAGAGGCTGGAGGAGAG
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/db_xref="taxon:9606"
/chromosome="16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCAAGTCCAGAGCACCCTGGGAGCCCTGGCTGCATGGGAACCCATAACCCAGTGCACG 60
                                                                                                                   GEGAAGETELA AAAR GETRIETGAAGACGTTCADUUAGUAGATCUAAGACGTGGAGTTT 420
                                                                                GAGAGGCTGGAGAAGGCCCTCCCTCAAGCGCTTTCGGGAGCTGGAGGAGGAGGTTC
                                                                                                                                                           ATCCAGACCGGGAGCTTCAACAGACAAGAGGGGGTGGTGGAAACGGCGCTACTCGGACTTC
                                                                                                                                                                                   ATCCAGACTGGGAGCTTTGACAACAACAACGCCGTCCTGGAACGGCGCTATTCCGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-JUN-2901) Membrane Biology Laboratory, Institute Mol & Cell Biol, 30 Medical Drive, Singapore 117609 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria, Rodenria, Sciurognathi, Muridae, Murinae, Mus 1 (bases 1 to 942)
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/db_xref="G1:14719305"
/db_xref="G1:14719305"
/td_xref="G1:14719305"
/td_xref="G1:14719305"
/translation="MASREHPGSPGWFGPINQCPTFTPQEVL,PPGPDLPCPGPEEAQD
/translation="MASREHPGSPGWFGPINGXLEXEVTYPTPQEVVIVIQTGS
GPSSNSSMTTRELOEHWQKEKSRWKHVRLLFEIASAFIEEKVSKEVMYQVVVIQTGS
GPSSNSSMTTRELOEHWQKEKSRWKHVRLLFEIASAFIELUSAETICERPPELFE
CDSDKAVVERRYSDFERDFIFFELFEARFGCT,PAGGYAALELLGBALLFLOEKLTAH
/CPSAAVPALCAALVCLFDELERFAEAFAVGEFALFCLFTRENHPYYAPLLDAMVPLAYA
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                 Submitted (05-331-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA on Cal 5, 1601 this sequence version replaced git.1072256.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submit+ad (02-UH, 2002) Geneme Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 260755)
McFherson, J.D. and Waterston, R.H.
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AC126054.2 GI:21639723
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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McPherson,J D and Wat
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus chromosome UNK clone RF23 298013, WORKING DRAFT SEQUENCE, 24 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Center project name. M_BA0298013
                                                                              Contact. submissions@watson.wustl.edu
                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                        Center code: WUGSC
                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                   Project Information
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Sequencing

Sequencing

vector:

M13; 0% plasmid; 100%

Summary Statistics

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 202000; agarose-fp
Insert size: 258455; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                  /chromosome="UNK"
/clone-"RP23-298013"
                                                                                            Location/Qualifiers
                                                organism="Mus musculus"/db_xref="taxon:10090"
                                                                                .26075
                                                                                                                                  164767: gap of unknown length
204254: contig of 39487 bp in length
204354: gap of unknown length
259423: contig of 55069 bp in length
                                                                                                         259523: gap of unknown length 260755. contig of 1232 bp in
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137947:
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1138: gap of unknown length
2235: contig of 1097 bp in length
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contig of 1539 k
gap of unknown l
contig of 1469 k
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of 2692
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of 2524
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of 5782
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of 2684
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of 1558
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of 17823 bp in length
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                                                                                                                                                                                 Db 105994
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                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                   Matches 536;
                                                                                                                                                                                                                                                                                                              Query Match 47.9%; Score 455.6; DB 2; Best Local Similarity 80.0%; Pred. No. 2.7e-53;
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                                                           CTGTGAGCGTCGGCGCGCCCTGCAGAGTACCTGGGCCTGCTCTACGCCATCCGCTGCGT
                                                                                                                                                 CATCGAAGACGTGGAGTTTCCCAGGAAGCACCTGACTGGGAACTTCGCTGAGGAGATGAT 461
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259524. .260755
/note="assembly_name:Contig8"
& 63869 c 62878 g 64428 t
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95043. .116513
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1139. .2235
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16747. .19438
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|38048. .164667
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116614. .137947
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19539. .24577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig41"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Kawai-Hio, Y., Satto, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomicsshri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI); supported by Japan construction: Helix Research Institute (HRI); supported by Japan (Construction: Helix Research Institute (HRI)); supported by Japan (Construction: HRI); supported by Japan (Construc
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Homo sapiens kidney cDNA to mRNA, clone_lib:KIDNE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFGSSB17 3270 bp mRNA linear Homo sapiens cDNA FL/131275 fis, clone FIDNE2026353
                                                                                                                                                                                                                                                                                                                    Evaluation; clone selection for full insert sequencing: RAB
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                                                                                                                                                                                                                               Location/Qualifiers
/tissue_type="kidney"
                                                                                               /db_xref="taxon.3606"
                                                                                                                                     /organism="Homo sapiens"
                                                    /clone="KIDNE2006353"
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o,J., Isono,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 GRACTTAGACACACACACAGTGGCCTGAGCTCCAGCATGACCACGCGGGGGAGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGGCACTTAGACACACAGTGGCCTGAGCTCCAACTCCAGCATGACCACGCGGGAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-JUN-2001) Membrane Biology Laboratory, Institute Mol & Cell Biol, 30 Medical Drive, Singapore 117609
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                                                                   /clone_lib="KIDNE2"
/note="cloning vector: pME18SFL3"
a 919 c 790 g 775 t
               RLGLDKRQSEARLQALQEAGLTPTPPPSLKELLIKEVLD"
                                 FLGHLQAVPELRHAPDLQDFFVLPELRRAQSLTCTGLYREALALWANAWOLQAOLGTP
SGPDRPLLTLAGLAVCHQELEDFGEARACCEKALQLLGDKSLHPLLAPFLEAHVRLSW
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                              /protein_id="AAK73126.1"
/db_xref="GI:14719307"
                                                                                                                                                                                                    /note="member of sorting nexim protein family"
/codon_start=1
                                                                                                                                                                                  product="SNX21"
                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                           'yene="SNX21"
                                                                                                                                                                                                                                                                               gene="SNX21"
                                                                                                                                                                                                                                                                                                                      db xref="taxon:9606"
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/db_xref="G1:21866801"
/translation="MHRGTQEGAMASPILHFLHALAGTGPGEAAASPEAEGFPESSE
/translation="MHRGTQEGAMASPILHFLHALAGTGPGEAGASPEAEGFPESSE
LEDDDAEGLSSRLSGTLSFTSAFDTEDDEDEDEDEDEAGPDQLLFLGEGTSGELAARTGPP
DGQMGSQLLARGLQDFWKKSRWTLAPGLLFEVTSAFTCDDFYNDDFYTAFTTAPTGAFGTP
DCQMGSQLLARGLQDFWKKSRWTLAPGLLFEVTSAFTSFAFEG
PDCQPAQISPPYSDEEDHFMLQDGPFGPMAAISFPKPLFDNFTAFTTAPSKAFEG
FLGHLQAVFELRHAPDLQDFFVLPELRFAQSLTCTGLYEEALALMAHAWGLGAGLGTP
SGPDRFLLTLAGLAVCHQELEDPGBARACCEKALQLGDKSLHPLLAPFLEAHVRLSW
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Submitted (15-MAY-2001) E-mail contact: humqueryesanger ac.uk
This cDNA sequence was assembled from public domain ESTs and single
pass sequencing reads from expressed DNA templates, aligned to the
genomic DNA sequence from the bacterial clone 337018 (AL008726).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1600)
Stavrides, G.S., Buckle, E.J. and Deloukas, P.
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FLGHLQAVPELPHAPDLQDFFVLPELFRAQSITCTGI.YPFALALMANAWQI,QAQLGTP
SGPDRPLLTLAGLAVCHQELEDPGEARACCEKALQLLGDKSLHPLLAPFLEAHVRLSW
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//product="hypothetical protein"
/product="hypothetical protein"
/proviein [il="GA739140 1"
/db_xref="GI:14149068"
/tcanslation="MHRGTQB9AMASBILHPI,PHAI,AGDGPGEAAASPEAEQFPESSE
LEDDDDAEGLSSETLSGTTS,ETTSAEDDEDDEDEDDEEAGPDQLFPLGDGTTSGEDABRSPPP
DGQWGSQLLARQLQDFWKKSRNTLAFQRLLFEVTSANVVKDPESKYVLYTLAVIGPGP
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join(15. .446,447. .515,515. .540)
/note="matches EST BE778315 from clone IMAGE:1866880"
                                                                                                                                                                                                                                                                complement(join(287. .353,355./note="matches EST AW748063"
/note="matches EST BF115410 from clone IMAGE:3570963"
                                                                                                                                                                                          matches EST AW954383"
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                                           join(529. .679,763. .784)
/note="matches EST T73159 from clone IMAGE:85952"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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BF569390 from clone IMAGE:4310245"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 ACGTGGAGTTTTCCCAGGAAGCACCTGACTGGGAGAACTTCGCTGAGGAGATGATCTGTGAGC 469
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                                                        TOTTOGAAGTGACCAGOGCTAACGTTGTCAAGGACCCGCCCTCCAAGTACGTGCTCTACA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACTGGCCTCTATCGTGAGGCTCTGGCACTCTGGGCCAATGCCTGGCAGCTGGAAGCCAAGCCC 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="matches EST AA365778" complement (1467. .1599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1327...1600)
/note="matches EST BF061958 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="matches EST AI301896 from clone IMAGE:1902265"
complement(join(1281. .1491,1503. .1600))
/note="matches EST AA868283 from clone IMAGE:1408418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1368.
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/note="matches EST AI400589 from clone IMAGE:2115843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="matches EST AW966060" complement(1148. 1600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="matches EST N56382 from clone JJ7526"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="matches EST AI097303 from clone IMAGE:1698216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="matches EST AW450013 from clone IMAGE:2735659"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="matches EST Z39581 from clone c-lea03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="matches EST F24584 from clone s4000015G12"
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53.1%;
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Pred. No. 9.6e-13;
0; Mismatches 317;
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RESULT 12
G67944/c
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source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Habib Zouali
Inflammatory Bowel Diseases
Centre d'Etude du Polymorphisme Humain (CEPH)
27, rue Juliette Dodu 75010 Paris, France
Tel: 00 33 1 53 72 50 20
Fax: 00 33 1 53 72 50 58
Email: habib@cephb.fr
Primer A: GGAACCAGAGTGAAAGAGG
Primer B: GCATCTCCCCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCCTGGCGCCTGGGCCTGGAC 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTTGGGGACAAGAGCCTCCACCCTTTGCTGGCACCCTTTCTGGAGGCCCATGTCCGGC 1062
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              Unigene EST cluster hs.87280; This STS contains a coding sequence which was identified by screening of Human cDNA library.

Location/Qualifiers
                                                                                                                                              Buffer:
Tris-HCl
                                                                                                                                                                                                                                                                                                                                                                                                                               30 cycles: 94 degrees C for 30 sec, annealing for 30 sec at 55 degrees C, extension at 72 degrees C for 30 sec; last extension at 72 degrees C for 7 min.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Association of NOD2 leucine-rich repeat variants with susceptibility to Crohn's disease Nature 411 (6837), 599-603 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hugot,J.P., Chamaillard,M., Zouali,H., Lesage,S., Cozard,J.P., Belaiche,J., Almer,S., Tysk,C., O'Morain,C.A., Gassull,M., Binder,V., Finkel,Y., Cortot,A., Modigliani,P., Taurent-Puig,P., Gower-Rousseau,C., Macry,J., Colombel,J.F., Sahbatou,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Frimates; Catarrhini, Hominidae, Homo. 1 (bases 1 to 270)
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IBD1prox-exonC genomic STS on chromosome 16q12:13 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activate AmpliTaq Gold,
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                                                                                                                                                                                                                                                                                                                                                                                                         PCR was carried out on Thermal Cycler (MJ Research, PTC-200).
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Polymerase : Taq Gold (Roche Perkin
                                                                                                                                                                                                                                                                    Taq Polymerase
                                                                                                                                                                                                                                                                                            Mgc12
                                                                                                                                                                                                                                                                                                                                          Primer:
                                                                                                                                                                                                                                                                                                                                                              Template (genomic DNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            denaturation step of genomic DNA at 95 degrees C for 12 min
                                                                                                                                50 mM
                                                                                                                                                                                                                                                           each 1 uM
each 200 uM
1.5 mM
0.05 units/ul
                                                                                                     8.3 at 20oC
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omo sapiens STS
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AGACACACAGTGGCCTGAGCTCCAACTCCAGCATGACCACGCGGGGAGAGCTTCAACTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 CTGGCAGAACCAGAAATGCCGCTGGAAGCAGGTCAAACTGCTCTTTGAGATCGCTTCAGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 CTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTTTTTGAGATTTGCTTTCAGC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 AGACACACAGTGGCCTGAGCTCCAACTCCAGCATGACCAQGAGGGGGGAAGCTTCAGCAGTA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
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                                                                                                                                                                                       Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics%hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanahe, T., Oraki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S., Yamamoto, J. Isono, Y., Kawai. Hio, Y., Salto, K., Nishikawa T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. MEDO, human JDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai, T. and Yama
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanigami,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone: HCHON2001099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligo capping; fis (full insert sequence).

Homo sapiens chondrocytes (HC) cDNA to mRNA, clone_lib.HCHON2
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                             /clone="HCHON2001099"
/cell_type="chondrocv+
/cell_type="chondrocytes (HC)"
/clone_lib="HCHON2"
                                                                                       /db_xref="taxon:9606
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Yamamoto, J.
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/db_xref="taxon:9606"
                                                                                                           organism="Homo sapiens"
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Pred. No. 7.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 ACGTGGAGTTTCCCCAGGAAG ACCTGACTGGGAGAACTTCGCTGAGGAGATGATCTGTGAGC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 GGG SAGETTE ACTACTES FAGALE ACTAGAATGCCGCTGGAAGCACGTCAAACTGC 229
                                                                                                                                                                                                                                         82 / TOGCCTACGCGCTGGGCANGGAC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $30 | СССЭЭЗАЭТТОСТУ) (ACTTOCTCACS)СЭССЭССЭЭЭДЭГТЭСЭСЭДСЭДСТТССЭСТЭСС 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 GTAGCCGGGCCTTTGAGCÁGTTTTTGGGTCACCTGCÁGGCAGGCAGCTGCCTGAGCTGCGCATG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538 CCATCTCCTTCCCCCCCAAAAAAAAAAAATTTTAATTACAĞAĞAĞCÇATTGÇÇÇGÇÇ 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.78 ACTCGGACTTTGAGAGGGACATGGCTGAAACCTGCAGGCAATGCGGGCCCAATGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 - СССАССВОЦАССТСКА ГОЗОСОВОВАН ЕПТГОВОВЗООВЗАВАВАВЕВЕССТВОЛЯЕ - 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 CGCCGCAGCTGCAGGATTTCTGGAAAJÁÁGTCCCGGAACAGCTTGGCAACCCCAGCGGCTGC 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCCGACTTCGCGAAGCTCCAGAAAGCGCTTGCTGAAGACGTTCAGGGAAGAGAGATCGAAG 469
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                                                                                                                                                                                                                                                                                                                                                       TGCTTGGGGACAAGAGCCTCCACCCTTTGCTGGGCACCCTTTCTGGAGGCCCATGTCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUTTUAGATUGUTTUAGUTUGUAT GAGGAGAAAAAGTUTUTAAGTTTGTGGTGTACC 289
                                         Homo sapiens cDNA FLJ34040 fis, clone FCBBF2005966. AK091359
              AK091359.1 GI:21749711
                                                                                               AK091359
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/db_xref="G1:21755195"
/db_xref="G1:21755195"
/translation="max15fprakelernetartiarrspafeqelghloavpriehap
DLQDPFVLPELPPAQSLTCTGLYPFALALMANAWQLOAQLGTESGPDRPLUTLAGLAV
CHOELEDPGEAPACCEKALQLLGDKSLHPLLAPFLEAHVPLSWPLGLDKPQSEAPLOA
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531. 1085
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52.4%;
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Pred. No. 5.
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                                                                                         CTCTC3CC3TTACTC33ACTTT3A4C33CTGCACC3AAACCTGCAGC33CAATTCC43GG-667
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                                                                                                                                                                                                                                                                                                                   TCTTCGAAGTGACCAGCGCTAACGTTGTCAAGGACCCGCCCTCCAAGTACGTGACAAACC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Karusa-Kamatari, Kisarazu, Chiba 292 0812, Japan (E-mail:genomicsahri.co.jp, Tel:81-438-52-3975, Fax:81 438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Bictechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.), 5'-6 3'-end one pass sequencing. FAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orsuki, T., Saro, H., Ora, T., Wakamatsu, A., 18011.5, Yamamoro, U., 18000, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, Y., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Muzakawa, K., Kanehori, K., Takahashi-Pujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Nagai, K., and Isogai, T., NEDO, human cDNA sequencing project
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF2
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Submitted (18-APR-2000) National Laboratory For Oncogenes
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road,
200032, People's Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazca; Chordata; Craniata, Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2064)
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Qin,W.X., Zhou,X.M., Zhang,P.P., Jiang,H
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AF258570.1 GI:10834685
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/db_xref="gi:10834686"
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/translation="MAAISFPRENERRNFTAETTAPPSPAFEQFLGHLQAVPELSWELGLDKRQSEARLQA
CHOELEDPGEARACCEKALQLL/GDKSLHPLLAPFLEAHVPLLSWELGLDKRQSEARLQA
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606 c 597 g 402
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317. .871
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Score 137.4; DB 9;
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Search completed. April 20, 2003, 15:50:04 Job time : 5691 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score 693.8	Query Match 73.0	Query Query Match Length DB ID Match 14 B0 73.0 934 14 B0 70.2 772 14 B0	DB 14	ID BQ706954 BQ230734	Description BQ706954 AGENCOURS BQ230734 AGENCOURS
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## ALIGNMENTS

FEATURES source		JOURNAL COMMENT	AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	KEYWORDS	ACCESSION	LOCUS DEFINITION	RESULT 1 BQ706954
Flate: LLCW.469 row. c column. 15 High quality sequence stop: 567. Location/Qualifiers 1934	mail: cgapbs-remail.nin.gov Tissue Procurement: Dr. Mark Watson CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Unpublished (1999) Contact: Robert Strausberg, Ph.D.	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 934)	human. Homo sapiens	EQ706954.1 GI:21845853	5', mRNA sequence. BQ706954	BQ706954 934 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8353554 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279494	

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/clone_lib="NIH_MGC_113"
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GCTTCAGCTCGCATCCAGGAGAGAAAAAGTCTCTAAGTTTTGTGGTGTACCAAATCATCGTC
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                                                                                                                                                         999CACTTAGACACACACAGT99CCTGANCTYCAANTYCANTATANCACAGAGGTT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Colone distribution information can be
found through the I M A G E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone="MAGE:6041672"
/clone="iba-WkH MGC 92"
/tissue_type="embryonal carcinoma, cell line"
/lab host="BH10B (phage resistant)"
/note="Organ. testis, Vector. pCMV-8PORT6, Site_1: Not1;
Site_2: Sall, Cloned unidit="tionally: oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH MGC Library."
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                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Tujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muzamatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-J84-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes fenome Pes 10 (10), 1617 1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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clone:9130017C17.
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                                                         Genome Res. 10 (11), 1757-1771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Pesearch (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail genome-res@jsc_riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:81-45-503-9216) Please visit our web site (http://genome.gsc riken.go jp/) for further details.
                                                                                                                                                                                                                                                                                               Rot = 185.2. Second strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to
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                                                                                                                       CTOSACTTOCTCACGOGGGACTOSOGGAGA TITTOGGCTGCCTGCGGGCCGGCCAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GUGAAGCTUCAFAAAAFYYSUYY TGAAFAYGTTVAJSFAFGAGATYGAAGACGTGGAGTTT 420
                                                                                                                                                                                                                                                    CTGCAGGAGTAACCTGGGCCCGGCCCCATACCCATACCGCTGGGCGCCGGCGAGAGTTC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAGGCTTGCATAAGTTCCTCCTCAAGCGCTTCGGGGCCGGAGCTGGAGGACGTGGCGTTC 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCEAGACTGGGAGTTTEGACAACAACAAGGCCGTGCTGGAACGGCGCTATTCGGACTTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTCAGCTCGCATCGAGAGAGAGAAAAGTCTCTAAGTTTGTGGTGTACCAAATCATCGTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACANGRAPIA PARAPAAR TRATTORY OF A GOOD AGACT TO CONTUTO CAGACOAGA - 282
                                                                              ATCCAGACCGGGACCTTCGACAGCGACAAGGGGGTGGTGGTGGAACGGCGCTACTCGGACTTC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOCTICAGO COGLATAGAGGAGAGAAAGTOTOCAAGTTTGTGATGTACCAAGTOGTGGTC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     755; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AGAAGCCCAAGATGGCCCCAGCTCTAACTCCAGCATGACCACAAGGGAACTC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGKDFAALQSPLDENQLPRPTHRDATLKELTVREYLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="cecum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
164._.1105
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/db_xref="GI:12858438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="MGD:MGI:1918857"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
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79.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 623.8, DB 11
Pred No. 1.9e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 GAGGGCCATCGCTACTATGCGCCTCTGCTGGACGCCATGGTCCGCCTGGCCTGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875 GAGGGGGGGAGGCCTCGGAGGCTGGGAGGGGGGGGGGTGGCTGGGAGAGGCGGC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAAGACTTCGTGACTCTGCAGGAGAGACTCTGGAGGACAAGACCAAGCTCCGGAGGCCCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW134842
UI-H-BI1-abs-e-09-0-UI-S1 NCI CC IMAGE:2713048 3', mRNA sequence.
AW134842
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCT-CGAP http://www.ncbi nlm nih gov/ncicgap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  information can be found through the I.M.A.G.E. Consurtium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer. M13 Forward
                                                                                                                                                                                                                                                                            /note="Vector: pr773D-Pac (Pharmacia) with a modified polylinker, Site 1. Not I, Site 2: Eco RI; The NCI CGAP Sub3 library is a subtracted library derived from the MCI CGAP Sub1 library, which is a subtracted library derived from the MCI CGAP Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI CGAP and interest NCI CGAP CO10, NCI CGAP Pr22, NCI CGAP F728, NCI CGAP CO10, NCI CGAP Exids, NCI CGAP Kidd1, NCI CGAP Kidd1, NCI CGAP Lym2, NCI CGAP Kidd3, NCI CGAP Kidd1, NCI CGAP Luci, NCI CGAP Brn23, NCI CGAP Luci, NCI CGAP Luci, NCI CGAP Brn23, NCI CGAP Luci, NCI CGAP Stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose common them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgapbs-r@mail.nih.gov
a driver whose composition is detailed below:

NCI CGAP Kid3 pool 1 LLAM 334-3337, 3682-3683,
3738-3853 (TMAGE Clonellus 1321376-1327)1, 1450-08-1455-7/5,
1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 338-3342,
3722-3725, 3776-3778 (TMAGE Clonellus 1321375-131583),
1471368-1472903, 1492104 1493255); NCI CGAP Lu5 pool 1
LLAM 3575-3582, 3881-3854 (TMAGE Clonellus 1414725-141793),
1520904-1522439); NCI CGAP GC4 pool 1
LLAM 3164-3167,
3716-3720, 3733-3735 (TMAGE Clonellus 141925-141793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:2713048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (Life Technologies)"
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REFERENCE
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                                                                                                                                                   DEFINITION
                                                      ORGANISM
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                                                                                                                                                                                                                                                               AGCTCACCGCCCACTGCCCTGCGGCCG 676
                                                                                                                                                                                                                                                                                                        G99009877AGTAGTAGTAGTAGTAGTAGTAGAGTTGCTGCTGCTGCTGCTGCAGGAGA 649
                                                                                                                                                                                                                                                                                                                                                                                                                                     ST09903030000T90A95ASTACCT996CCTSCTCTACGCCATCCGCTGCGTGCGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCGGGAGCTICAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGTGGAGTTTCCCAGGAAGCACCTGACTGGACTTCGCTCAGGAGATGATCTGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCCGACTTCGCGAAGCTCCAGAAAGCGCTGCTGAAGACGTTCAGGGAGGAGGAGTCGAAG
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                                                                                                                                                                                                                                              AGCTCACCGCCCACTGCCCTTGCGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCGGGAGCTTCAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGC 448
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eurheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 540)
                                                  Homo sapiens
                                                                                                                             mRNA sequence
                                                                                                                                              wg97a05 x1 NCI_CGAP_Kid11 Hcmo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                      244 TCAGETEGFATEGAGAGAGAGAGAGAGAGTTTGTGGGGGGTACGAAATGATGGTGATG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop. 472.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by. Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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  96
                                                                                                            purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs
                                                                                                                                                                               /note="Organ: kidney; Vector. pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1. Not I, Site 2. Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
                        Fatima Bunaldo.
                             1492104-1493255). Subtraction by Bento Soares and M. Fatima Bunaldo. "
                                                                  from a pool of 5,000 clones made from the same library (clunerDs 1323912-1325831, 1471368-1472903 and
                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                             prepared, and ss circles were made in vitro. Following HAP
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                clone="IMAGE.2873213"
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149 g
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Best Local Similarity Matches 504, Conserv

Conservative

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Score 491.8; DB 1 Pred. No. 8.2e-90; C, Mismatches 2

DB 10; Length 506;

Gaps

51.7%; 99.4%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AICC4982 478 bp mRNA linear EST ouC7aO9.xl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone IMAGE:1625560 3', mRNA sequence.
                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. Insert Length: 791 Std Error: 0.00 Seg primer: primer name ambiguous.
                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                              NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Mammalia; Eutheria;
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHl19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in
                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:1625560"
/clone=1b="Soares NFL_T_GBC_S1"
/lab_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIIll1 row: a column: 11
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 671)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driving PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 lbraries. The pools consisted of 1.M A.G. E. clones 297480.302897, 682632.68779, 726438-728711, and 729986-731399. Subtraction by Bento Soares and M. Fattma Bonaldo. "
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99.0%;
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Fred. No. 2.1e-85;
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/lab_host="DH10B (TI_phage-resistant)"
/note="Organ: kidney; Vector: pcMV.SPOPTG; Site 1, Not1,
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies, Note: this is a NCI_CGAP Library. | "
a 235 c 240 g 95 t
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Query Match 48.4%; Score 460; DB 9; Best Local Similarity 100.0%, Fred. No. 2.2e 83
TGCTGAAGACGTTCAGGGAGGAGATCGAAGACGTGGAGTTTCCCAGGAAGCACCTGACTG
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                                                                                                                                                                                        TSCTCTACSCCATCCSCTSCTSCSCSCSCTCCCSSSAGTTCCTSGACTTCCTCACSCSSC
                                                                                                                                                                                                                                                                                                GGAACTTCGCTGAGGAGATGATCTGTGAGCGTCGGCGCCCTGCAGGAGTACCTAAACC
                                                                                                                                                                                                                                                                                                                                          GSAACTTCGCTGAGAGATGATCTGTGA 9 CEC COSCGGCCCTGCAGGAGTACCTGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGATCGCTTCAGCTCGCATCGAGG 259
                                                                                                                                                 TGCTCTACGCCATCCGCTGCGTGCGCCGCTCCCGGGAAGTTCCTGGACTTCCTCACGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGAAAAGTCTCTAAGTTTGTGGTGTACCAAATCATCGTCATCCAGACTGGGAGCTTTG
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Eukarycta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostom
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 460)
NCT-CGAP http://www ncbi nlm.nih gov/ncicgap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Email: cgapbs-Temail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image lln] gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="DH108"

//lab host="DH108"

//note="Organ. pooled, Vector. pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I, Site 2. Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCP-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of IM A G E clones 997480 302987, 682420 487239, 726438-72871; and 72296 731199. Saltractically Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                      193 CAGAACCAGAAATGCCGTEGAAGCACGTEGAAACTGCTTTTGAGATCGCTTCAGCTCGC 252
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                                                                                                                                                                                                                                                                                                400
CTGACTGGGTAACTTCGGT5AGGAGGATGATCTGTGAGGGTGTGGGCGCCCTGCAGGAGTAC 492
                                                                                                                                                                                                                                                                                                                                ATCGAGGAGAGAAAGTCTCTAAGTTTTGTGGTGTACCAAATCATCGTCATCCAGACTGGG 312
                                                                              AAAGOGOTGOTGAAGAOGTTOOAGGAGAGATGGAAGAOGTGGAGTTTCCCCAGGAAGCAC 221
                                                                                                                         AAAGCGCTGCTGAAGACGTTCAGGGAGGAGGAGCGAAGACGTGGAGGTTTCCCAGGAAGCAC 432
                                                                                                                                                                                         AGCTTTGACAACAACAAGGC
                                                                                                                                                                                                                                     AGCTTTGACAACAACAAGACCSTCCTGGAACGCCCTATTCCGACTTCGCGAAGCTCCAG 372
                                                                                                                                                                                                                                                                                     ATCGAGGAGAAAAGTCTCTAAGTTTGTGGTGTACCAAATCATCGTCATCCAGACTGGG 341
                                                                                                                                                                                                                                                                                                                                                                                         CAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGATCGCTTCAGCTCGC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460;
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AK59241.x1 Scares_NFL_T_GEC_S1 Homo sapiens cDMA clone IMAGE.2934644 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information. Possible reversed clone: polyT not found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Location/Qualifiers
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
High quality sequence stop: 460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-ramail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Scares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 795 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 461)
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                                                                                              Similarity
                                                                          Conservative
                                                                                                                                                               /clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2117846"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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100 0%; Fr
                                                                                        Score 460; DB 9;
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sapiens cDNA clone IMAGE:2117846 3',
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RESULT 13
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infowimage.llnl.gov) for further information. Seq primer: -40ml1 fwd ET from Amersham High quality sequence stop: 442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Pobert Strausberg, Ph.D
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7773 vector (Pharmacia). Library went through accounty.
                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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/clone=lib="Soares_fetal_heart_NbHH19W"
/cos="The Coares_fetal_heart_NbHH19W"
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                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazca, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                High quality sequence stop: 408
                                                                                                                                                                                                                    Possible reversed clone: polyT not found
                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image_llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
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/clone_lib="Soares_NFL_T_GBC_S1"
//lab_host="DH10B"
/note="Organ: pooled, Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:2911527"
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                                                                                                                        /organism="Homo sapiens'
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te50d05.x1 Scares NFL T GBC $1 Homo
IMAGE:2090121 3', mRNA sequence.
Mammalia, Eutheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 500)
NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                Homo sapiens
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Similarity 99.6%;
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Pred No. 1.6
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sapiens cDNA clone
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COMMENT

Search completed: April 2n, Job time : 3723 secs

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Seq primer:

-40UP from Gibco

SOURCE KEYWORDS VERSION

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23 Acceccicacinecconecescosc 1
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/lab_host="DH108"
/lab_host="DH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker, Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19%, trestis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools consisted of
IM_A_GE_clones_2374AC_337287_62532_687233,
IM_A_GE_clones_2374AC_337287_62532_687233.
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Soares and M. Fatima Bonaldo. "
155 c 154 g 96 t 1 others
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries
1: | SIDS1|gcgdata|geneseq|geneseqn-embl|NA1980.DAT: *
2: | SIDS1|gcgdata|geneseq|geneseqn-embl|NA1981.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No. 1 1	Score 951 949.4 817.6	Query Natch Length DB 100.0 951 22 99.8 1315 22 86.0 1317 23	Length 951 1315	DB 222 233	i H	Description  Nucleotide sequence Nucleotide sequence DNA encoding novel
₽	951	100.0		10	AAI65832	Nucleotide
N	949.4	8.66		2	AA165593	Nucleoti
w	817.6	86.0		23	AAS84164	DNA enco
4	670	70.5		22	AA165594	Nucleotide seguenc
un	506	53.2		23	AAS78753	DNA encoding novel
0	354	37.2		24	ABQ18060	Oligonucleotide fo
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AAV19860	AAV19861	AAV19863	AAV19864	AAV19862	AAQ98470	AAT80414	AAT78508	ABL68935	C1	AAT93095	AAQ50511	AAT16766	AAQ43032	AAS08693	195		AAA09686	AAD17186	w	551	217	215	2722	44	717	30.5	ω,	356	816	872	(n	564	AAL45648	AAC77276	AAK61789
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### ALIGNMENTS

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ARESULT 1
AA165832
ID AA16
XX AA16
AC AA16
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Nucleotide sequence of a human PSGL-1 binding protein.

Human, F selectin glycoprotein ligand binding protein;
PSGL-1 binding protein; selectin ligand interactor cytoplasmic-1 protein;
SLIC-1 protein; signal transduction; cytoskeletal organization;
immune response; inflammatory response; cell adhesion, cell migration;
cell activation; cell growth; cell differentiation; cell proliferation; immune system disorder; cardiovascular disorder; haematopoietic disorder; thrombotic disorder; ss.

Homo sapiens.

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1..951
/*tag= a
/product= "P-selectin glycoprotein ligand (PSGL-1)
    binding protein"
                                                                                Location/Qualifiers
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W0200173028-A2

04-0CT-2001.

23-MAR-2001, 2001WO-US09469.

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Best Local:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intra-cellular communication, adhesion, migration, cell activation, growth, differentiation and proliferation. The SLIC-1 proteins provide novel diagnostic targets and therapeutic agents to control or modulate SLIC 1 molecule associated disorders such as an inflammatory or immune system disorder, a cardiovascular disorder, a cellular proliferation, activation, adhesion, growth, differentiation or migration disorder or a haematopoietic or thrombotic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to regulate a variety of cellular processes such as signal transduction, cytoskeletal organization, immune and inflammatory responses, inter- and intra-cellular communication, adhesion, migration, cell activation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotides (SLIC-1) which encode novel P-selectin ulcoprotein ligand (PSGL-1) binding protein, useful as targets for developing modulating agents to regulate a variety of cellular processes including signal transduction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PSGL 1) binding protein. The protein is a member of the selectin ligand interactor cytoplasmic (SLIC-1) family. The SLIC-1 polynucleotides and polypeptides are useful as targets for developing modulating agents
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                             CTGCAGGAGTACCTGGGCTGCTGCTTAAGGCATACGCATTCCCTGCGGGGAGTTCCCGGGGAGTTC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | CCCAGGAAGCAC||T\3A\T\33\3AACTT\C3\T\3A\3A\7A\T\3A\7\T\T\T\3A\0\C\T\7\GG\C\C\C\C\
                                                                                                                                                                             GOGAAGCTOCAGAAAGCGCTGCTGAAGACGTTCAGGGAGATCGAAGATCGAAGTTT
                                                                                                                                                                                              GCGAAGCTCCAGAAA W TY TYGATGAAGACGTTCAGGGAGGS/SATCGAAGACGTTGAGTTT 420
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RESULT 2
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                                                                                                                                                   New human nucleic acids associated with intestinal inflammatory disease, useful for diagnosis, prognosis and control of these d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; inflammatory bowel disease 1 protein; IBD1, IBD1prox; intestinal inflammatory disease; apoptosis; NF-kappa B; cancer; inflammatory disease, immune disease, cryptogenetic inflammation;
                                                                        Claim 1; Page 72-73; 97pp; French.
                                                                                                                          also related proteins
                                                                                                                                                                                                                                       P-PSDB; AAG79120.
                                                                                                                                                                                                                                                                                                                  Huget JF,
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                                                                                                                                                                                                                                                                                                                  Thomas G,
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The present sequence encodes a human The IBD1prox protein is in proximaty

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protein designated IBD1prox.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bowel disease 1 (IBD1) protein, which is associated with intestinal inflammatory disease. The IBD1 gene is probably involved in regulation of approssis and activation of Mr kappa B. The IBD1 and IBD1prox polynucleotides are is useful as source of probes and primers, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Semience 1315 BP; 257 A; 419 C, 394 G, 245 T, 0 other,
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                   GACCGCCCCCCGAGGCCTTCGCGGGCCGGAAGAGGGCCTGCAGCCCTGCAGCCCCGG
                                                                                                                                     TACCCGCGCGCCCTGGAGCTGCTGCTGCGCGTGCTGCCAGGAGAAGCTCACCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAGGAAGCACCTGACTGGGAACTTCGCTGAGGAGATGATCTGTGAGCGTCGGCGCGCCC
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                                                                                                   COCAGGAAGCACOTGACTGGGAACTTCGCTGAGGAGATGATCTGTGAGCGTCGGGGGGGCCC 650
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            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
P-PSDB; ABG19977.
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS84164 standard; cDNA; 1317
       at ftp.wipo.int/pub/published_pct
                                                                                                                                                                                                                 Claim 1; SEQ ID No 19968; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #19968
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                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping, gene mapping, gene therapy, forensic; sood supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                     || (GCA434)|| (CCA3443434)|| (ATO 5"TACTATOCOCCTCTSCTGGACGCCATCATCCGCCTGG-829
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                                                                                                                                                                                                                                                                                                                                                                                                                              ACCGCGACCTCGACCGCCTGCGCGCGAGGGCCCTTCGCGGCGGAGAGAGGGGCCCTGCAGCGCC
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97.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA165594,
                                                                                                                                                                                                                                                                                                                                             New human nucleic acids associated with intestinal inflammatory discase, useful for diagnosis, prognosis and control of these d
                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAG79120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR 2000, COOCER-0003832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chamaillaid M;
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The present sequence encodes a human protein designated IBD1prox. The IBD1prox protein is in proximaty to a gene encoding inflammatory bowel disease 1 (IBD1) protein, which is associated with intestinal inflammatory disease. The IBD1 gene is probably involved in regulation of approxis and activation of NF-kappa B. The IBD1 and IBD1prox polynucleotides are is useful as source of probes and primers, as source of (anti)sense oligonucleotides, for recombinant production of polypeptides, and in screening for interactive compounds. The polypeptides are used to raise specific antibodies which useful for polypeptides are used to raise specific antibodies which useful for polypeptides detection or purification of IBD1 and IBD1prox, to screen

Claim 1; Page 75-77; 97pp; French.

related proteins

of these diseases

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RESULT 5
AAS78753
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Human; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                             AAS78753 standard; cDNA; 806
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                                                                DNA encoding novel human diagnostic protein #14557.
                                                                                                                                        13-FEB-2002
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                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for identifying expressed genes. (I) is useful in gene through techniques (II) or to treat disease states involving (III) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical contemporary of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations contemporary of the polypeptide and polynucleotide sequences have applications in CC diagnostics, for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content for the printing intimation, but was obtained on electromic format directly from WiPO as the print of the printing of the product of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 806 BP; 169 A; 165 C; 139 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, SEQ ID No 14557; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2000;
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240 CGC-TTCAGCTCGCATCGAGGAGAGAAAAGTCTCTA-AGTTT5TGGTGTACCAAATCATC
                                                                                                                                                                                                                                                                                               176 GCAAGGACCCAGCAGGCACCACTGGCCACCGACCTCCCCAGGACCTCAGGACCTGAC
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                                                                                 TCAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGÇACGTCAAACTGCTCTTTGAGAT
                                                                                                                                                                                           AGGCACCTGCCCCCACACAGTGGAATAAAATACAAACTCCAGCATGACCACGCGGGGAGCT
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              С,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 506; DB 23;
Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug; side effect; cancer; central nervous system; cardiovascular; qastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ18060 standard; DNA; 570
                                                                                 Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                             07
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, cytosine methylation, 5' TpG-3', uracil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for detecting cytosine merhylation SEQ ID NO 4651
                                                                                                                                                                                 WPI; 2002-371829/40
                                                                                                                                                                                                                                                                                             01-SEP 2600; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                             W0200218632-A2
                                                  This invention describes a novel method for determining the degree
                                                                                                                                                                                                                                                                               05 SEP-2000; 2000DE-1044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGTCACCGCCCACTGCCC 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COGGGAGTT - COTGGACTTCCTCACGCGGGCGGGGGAGGCTCTTCG-GCTGCCTG
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                                                                                                                                                                                                                                               EPIGENOMICS AG
                                                                                                                                                                                                               Piepenbrowk C, Berlin K,
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The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cyrosine methylation described in the disclosure of the invention.
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Pred No 1 4e-56;
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# ABQ18061 standard; DNA; 570 BP

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12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 4652

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                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, rardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation. The method allows the completion status of many C residues to be determined simultaneously. ABO13410-ABQ54121 represent genomic DNA sequences used to illustrate the cut the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                   Matches 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytosine methylation; 5'-CpG 3', uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 570 BP; 216 A; 202 C; 62 G; 90 T, 0 other;
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                                    This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ18058 standard; DNA; 570
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The method allows the methylation status of many of residues to be determined simultaneously. AB014410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                              Human; cytosine methylation; 5'.CpG 3'; uracil, cytosine; diagnosis, drug; side effect; cancer; central nervous system; cardiovascular; qustrointestinal; respiratory system, single nucleotide polymorphism
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Romo sapiens.
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Sequence 570 BP; 230 A; 197 C, 62 G, 81 T, 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK61789 standard; cDNA; 588
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                            example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of hæmatopoietic-derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 588 BP; 140 A; 166 C; 167 G; 105 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                       to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
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                                                                                                                                                                                                                    Local Similarity
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Pred. No. 1.8e-43,
                                                                                                                                                                                                                                     DB 22,
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Claim 5;

Page 4838; 5507pp; English

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human CRFX open reading frames 1 to 3161. The CRFX

sequences have activities such as: cytostatic; hepatotropic; vulnerary

antipsoriatic, antiparkinsonian, nootropic; neuroprotective;

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02-APR-1999;
05-APR-1999;
30-MAP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antianaemic, gene therapy, cancer, proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease, diabetes mellitus; hypothyroidism, SCID, AIDS; cholesterol ester storage, systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn, wound; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage, cartilage damage; antiinflammatory disease; coagulation;
                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO US08621.
                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08 FEB:2001 (first entry)
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                                                                                                                                                                       P-PSDB; AAB43067.
                                                                                                                                                                                                                  Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral, antibacterial, antifungal, antirheumatic, antithyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF2831 polynucleotide sequence SEQ ID NO:5661
                                                                                                                                                                                                                                                                                                                                 31-MAP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis; contraceptive; ss.
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99US-0127728
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RESULT 12
AAL45648
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AC AAL45
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XX Human
XX Unide
CS Unide
FH Key
FH CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                               Human; cancer cell growth inhibitor; cancer; cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                           Human cancer cell growth inhibitor related cDNA SEQ ID NO: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-2002
(SHAN-) SHANGHAI CITY INST ONCOLOGY
                                       18-MAY-2000; 2000CN-0115744.
                                                                             18-MAY-2000;
                                                                                                                       05-DEC-2001.
                                                                                                                                                           CN1324819-A.
                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL45648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids can be used to express ORFX proteins in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteopathic; anticonvulsant; antiarthritic; immunosuppressant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGCTCGCATCGAGGAGAGAAAAAGTCTCTAAGTTTGTGATG 360
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                                                                             2000CN-0115744
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                       Location/Qualifiers 317..871
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/product= "cancer cell
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99.3%;
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Pred. No. 8.6e-41;
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AAL45649
ID AAL4
XX
AC AAL4
XC II-J
XX
DE Huma

AAL45649 standard; DNA; 2064 BP

AAL45649; 11-JUN-2002

(first entry)

Human cancer cell growth inhibitor related DNA SEQ ID NO:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2064 BP; 459 A; 606 C, 597 G, 402 T, 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human protein, and the polynucleotide that encodes it, useful for inhibiting cancer cell growth \ \ \text{-}
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                                819 GGTCCGCCTGGCCTACGCGCTGGGCAAGGAC 849
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TGTCCGGCTCTCCTGGCGCCTGGGCCTGGAC
                                                                CCTGCAGCTGCTTGGGGACAAGAGCCTTTTACTTGCTGGTACCCTTTTCTTGGAAGCCCA, 7×s
                                                                                                  CCTGCAGCGCCTGCAGGCCCGGGAAGGGCCATCGCTACTATGCGCCTCTGCTGGACGCCAT
                                                                                                                                  GGCCGTGTGCCACCAGGAGCTTGGAAGACCCTTGGAGAGGCCCGGGGGCATGCTGTGAGAAGGC
                                                                                                                                                                                                      GCAGGAGAAGCT---CACCGCCCACTGCCCTGCGGGCGGCCGGGCCCTGIGCGCCGI
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53.8%;
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Pred. No. 1.3e-16;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human proteins capable of acting as cancer cell growth inhibitors. These can be used to inhibit cancer. The present sequence is a coding sequence described in the exemplification of the invention.
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P-PSDB; AAO17131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000; 2000CN-0115744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel
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pred No 1 3e-16;
p; Mismatches 261; Indels 3;
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19:MAY 2000,
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24 FEB:2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy.

ARS:18161-ARS:28764 represent genomic sequences encoding for novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human respiratory antigens.

Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and CONA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis -
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                                                      TGCCCGCCGTASCCGGGGCTTTGAGCASTTTTTGGGTCACCTGCAGGAGGAGTGCCTGAGCT
                                                                                                       CTGTGASCETTGECÇCCTGCACAÇETACCTSASCCTGCTCTACGCCATCCGCCGCCGC
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                                                                                                                                                                                                                 GATCGAAGACGTGGAGTTTCCCAAGGAAGCACCTGACTGGGAACCTTCGCTGAGGAGATGAT
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Barash SC, Ruben SM;

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

Disclosure; SEQ ID NO 42060; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) croteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) considered the colds may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, and diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic seguences from the present invention. AAK54942 to AAK54950 and AAM82169 concers at the present invention. represent sequences used in the exemplification of the present invention

Sequence 23580 BP; 5938 A; 5961 C; 5927 G; 5754 T; 0 other,

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                                                 Query Match
Best Local (
                                Matches 306; Conservative
281 GOTGTACCAAATCATCGTCATCCAGACTGGGAGCTTTGACAACAACAAGACCGTCCTGGA 341
                                                   Similarity
                                              14.3%;
53.6%;
                                Score 135.8; DB 22; Length Pred. No. 2.9e-16; 0; Mismatches 262; Indels
                                                             Length 23580;
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Search completed. April 20, 2003, 15.57:11 Job time: 975 secs

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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications NA:*

1: /cgn2_6/ptodata/l/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/l/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/l/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/l/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/l/pubpna/US07_NEW_PUB.seq:*

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11: /cgn2_6/ptodata/l/pubpna/US10_PUBCOMB.seq:*

12: /cgn2_6/ptodata/l/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/l/pubpna/US09_PUBCOMB.seq:*

14: /cgn2_6/ptodata/l/pubpna/US60_NEW_PUB.seq:*
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2481 398 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

## ALIGNMENTS

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US-09-816-697-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: LOFENZ, M., et al.

TITLE OF INVENTION: A NOVEL P-SELECTIN GLYCOPROTEIN LIGAND (PSGL-1);

TITLE OF INVENTION: BINDING PROTEIN AND USES THEREFOR

FILE REFERENCE: GEN-5380

CURRENT APPLICATION NUMBER: US/09/816,697

CURRENT FILLNG DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/192,104

PRIOR APPLICATION NUMBER: 60/192,104

PRIOR APPLICATION DATE: 2000-03-24

NUMBER OF SEO ID NOS: 4

NUMBER OF SEO ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09816697 ; Patent No. US20020037840A1
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US-09-816-697-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 9:
                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 951; DB 10; Length 951; Best Local Similarity 100.0%; Pred No 6 1e-233; Matches 951; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                  181 CAGCAGTACTGGCAGAAACCAGAAATGCCGCTGGAAGCAGGTCAAACTGCTCTTTGAGATC
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                                                                                                                                                                                                                                            SEQ ID NO 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 990, Application US/09764860 Patent No US2002004953A1
Mat ches
                                       Best
                                                             Query Match
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                             LENGTH: 23580
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       Matches 235,
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                                       Query Match
Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZJ2
FILE REFERENCE: PTZJ2
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CURRENT FILING DATE. 2001-01-17
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Publication No. US20020182669A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Matches
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CURRENT FILING DATE: 2001-05-17
PPIOP APPLICATION NUMBER: CA 2,766,241
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TITLE OF INVENTION: GPI-Anchored Small Leucine-Pich Proteoglycan Gene NYX
FILE REFERENCE: 45499-2
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SOFTWARE: PatentIn version 3 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Bech-Hansen NT et al.

TITLE: Mutations in NYX, encoding the leucine-rich proteoglycan nyctalopin,
TITLE: cause X-linked complete congenital stationary night blindness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 319-323
DATE: 2000-11-01
DATABASE ACCESSION NUMBER: GenBank / AF254868
DATABASE ENTRY DATE: 2000-12-23
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ORGANISM: Mus sp.
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Fred. No. 8.6e-05,
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CURRENT FILING DATE. 2001 03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE. 2000-03-21
PRIOR PAPPLICATION NUMBER: 69/206,848
PRIOR FILING DATE. 2000-05-23
PRIOR APPLICATION NUMBER: 69/207,727
PRIOR APPLICATION NUMBER: 69/207,727
PRIOR FILING DATE. 2000-05-26
PRIOR FILING DATE. 2000-05-26
PRIOR FILING DATE. 2000-05-26
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LENGTH: 7419
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                                                                                                                                                                                                                            Best Local Similarity
Matches 129, Conserv
                                                                                                                                                                                                                                                      Query Match
Best Local
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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PRIOR FILING DATE: 2000-10-23
FRIOR AFFLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/257,931
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733 GAGGCCTTCGCGGGCGGAAGAGAGACACCTTR-WARRONGSAAGAGCATCGC T92
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RESULT 7

991-495-115/c

; Sequence 115, Application US/03874923 ; Patent No. US20020081320A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G. APPLICANT: Campos-Neto, F. APPLICANT: Webb, John R.

Antonio

APPLICANT: APPLICANT:

Dillon, Davin C. Skeiky, Yasir A.

Bhatia, Ajay

APPLICANT:

US-09-874-923-115/c

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LENGTH: 7065
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APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND BIAGNOSIS OF LEISHMANI
FILE REFERENCE: 210121.42009
CURRENT APPLICATION NUMBER: US/09/991,496
CUPPENT FILING DATE: 2001.11-20
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1480 CCTCGTC 1474
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Coler, Rhea
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US-09-976-059-1
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION Genes and Proteins for Riosynthesis of Paroplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CUBRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                 SEQ ID NO 1
LENGTH: 88
TYPE: DNA
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LENGTH: 7065
TYPE: DNA
OPGANISM: Leishmania major and chagasi
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APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANI
FILE REFERENCE: 210121.420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS. 122
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                                                                       ORGANISM: Actinoplanes sp
FEATURE:
NAME/KEY: misc_feature
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nes 193;
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NAME/KEY: misc_feature
LOCATION: (70099)...(70662)
OTHER INFORMATION: ORF 18; p
NAME/KEY: misc_feature
IOCATION: (70659)...(71906)
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OTHER INFORMATION: ORF 15; F
NAME/KEY: misc feature
LOCATION: (66546)...(67370)
OTHER INFORMATION: ORF 16; F
NAME/KEY: misc feature
                                            OTHER INFORMATION: ORF 22;
NAME/KEY: misc_feature
LOCATION: (75535)...(76464)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: ORF 17;
NAME/KEY: misc feature
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OTHER INFORMATION: ORF 8; negative strandedness NAME/KEY: misc feature LOCATION: (13617)..(12802)
                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (74216)...(73563)
OTHER INFORMATION: OPF 21;
                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (73439)..(71964)
OTHER_INFORMATION. OFF 20;
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LOCATION: (15880)..(19035)
OTHER INFORMATION: OFF 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: ORF 5; negative strandedness NAME/KEY: misc_feature LOCATION: (9464)..(8130) OTHER INFORMATION: ORF 6; negative strandedness NAME/KEY: misc_feature
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LOCATION: (6665)..(5814)
OTHER_INFORMATION: ORF 4; negative
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LOCATION. (39713)...(65800)
OTHER INFORMATION OPF 14;
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LOCATION: (19032)..(39713)
CTHER INFCRMATION. ORF 13;
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LOCATION: (4038)..(504)
                                                                                                                             NAME/KEY: misc_feature
LOCATION: (75424)..(742
                                                                                                                                                                                                                                                                                            LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19;
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LOCATION: (15591)..(15
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LOCATION: (15203)..(13614)
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LOCATION: (3118)..(4032)
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OTHER INFORMATION: ORF 1; positive strandedness
                      NAME/KEY:
                                          OTHER INFORMATION: ORF 23;
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(9691)..(107)
misc_feature
(78110)..(76449)
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US 08 957-425-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/08957425 Publication No. US20030069401A1 GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 136; Conservative
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LOCATION: (87494)...(88420)
OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (87372)...(86803)
OTHER INFORMATION: ORF 32; positive strandedness
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LOCATION: (85556) (86885)
OTHER INFORMATION: OPF 31; positive
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LOCATION: (84481)..(85548)
OTHER_INFORMATION: OPF 30; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (825\overline{8}7)...(84446) OTHER INFORMATION: OPF 29; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (81909)..(81682)
OTHER INFORMATION: OPF 27; negative strandedness
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LOCATION: (79864) ... (78107)
COTHER INFORMATION: LOCATION 25; negative strandedness
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LOCATION: (82587)..(844
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LOCATION: (H2346)..(82
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LOCATION: (81624), (79)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 GAGGGCCATCGCTACTATGCGCCTCTGCTGGAGACGC 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match
Local Similarity 49.5%;
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33
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                                                                                                                                 CITY: BOSTON
                                                                                                                                                                                        ADDRESSEE: TESTA, HIRWITZ & THIBEAULT STREET: 53 STATE STREET
COUNTRY: U.S.A.
                                                             STATE: MASSACHUSETTS
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RUEGER, DAVID C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OZKAYNAK, ENGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THANGAVEL
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Best Local Similarity 48.8%; Pred. No. 0.00034; Matches 141; Conservative 2 Microschit
                                                                                     08-957-425-28
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFONE. 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                    OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN" /product- "hOP2-PP" /note- "hOP2 (cDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   LOCATION.
                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1723 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEFERENCE/DOCKET NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 179,460 FILING DATE: 08-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 232,630 FILING DATE: 15-AUG 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 315,342 FILING DATE. 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 660,162 FILING DATE: 22-FEB-1991
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                                                                                                                                                                                                                                            TISSUE TYPE: HIPPOCAMPUS
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APPLICANT: Broughton, William John
TITLE OF INVENTION Genomic Sequence of Phizobium Sp. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
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APPLICANT: Perret Xavier i
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Pred. No. 0.00085;
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APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: APPLICANTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SCFTWARE. FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
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GENERAL INFORMATION.
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SEQ ID NO 1
LENGTH: 15872
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CURRENT APPLICATION NTMBER: US/03/560,846
CURRENT FILING DATE: 2001-05-18
PPIOP APPLICATION NUMBER: 09/105,537
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Pred. No 0 0014;
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Best Local Similarity 49.1%; Pred, No. 0.0014;
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CURRENT APPLICATION NUMBER: US/10/076,157
CURRENT FILING DATE: 2002-02-15
PRIOP APPLICATION NUMBER: US 09/212,247
PRIOP FILING DATE: 1998-12-16
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APPLICANT: Jimenez, Alberto;
APPLICANT: Garcia, Maria Ang
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APPLICANT: Suelberger, Harald
APPLICANT: Joeffken, Hans Wolfgang
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SOFTWARE: WordPerfect v. 6.1
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TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use the
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LOCATION: 1478..2592
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    594 ООНОСЛЕТАСОСОВОТОТОТАКА ТЕПТОТЕОТОТОТОТОТОТОТОТОТОТАКАТЕЛЕГА.

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                                                                                                                                                                                                                                                          474 GOOGSCCCTOMA HARIAACTOJOGGCTOMPHACHCHATROCHATROCHACH NA TEORG 533
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US. 09-796-679-5/c
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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: PCT/NZ97/00040
PRIOR FILING PATE: 1997-03-27
PRIOR APPLICATION NUMBER: NZ 286284
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
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APPLICANT: University of Otago
TITLE OF INVENTION: Parapoxvirus vectors
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ORGANISM. Orf virus strain NC-2
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                                                                                                                                                                   CONFIDENCIA DA GARCITO DE CONTRO DE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 4020
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Search completed: April 20, 2003, 20:19:49 Job time : 664 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                Database
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Perfect score:
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951
Issued_Patents NA:*

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(cgn2_6/ptodata/2/ina/5B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/backfiles1.seq:*
(cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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uence 20, A	equence	equence 20, A	equence 20, A	e 20, F	equence 7,	equence 7, App	equence 20,	nce 3, 🏞	equenc	equence 10,	e 28,	equence 11,	Sequence 11, Appl		equence 48	e 1,	(1) (1)	equence 4,	nce 6,	Sequence 8, Appli	equence 5,	e 1,	nce 1,	equence 1,	e 7,	Sequence 50, Appl	Description		

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Sequence 20, Appl	Sequence 20, Appl	<b>"</b>	, 01	Sequence 7, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 5, Appli	-	sequence 20, Appl	Sequence 20, Appl	Sequence 28, Appl	Sequence 28, Appl	7, 1	Sequence 20, Appl	Sequence 5, Appli	Sequence 20, Appl	Sequence 20, Appl

### ALIGNMENTS

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                                                                                                                                                                      US-08-642-255-50
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                                                                       Query Match 6.0%; Score 56.6; DB 1; Length 756; Best Local Similarity 46.3%, Fred. No. 0.002, Matches 202; Conservative 0; Mismatches 254; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                     NAME: ROWLAND, Bertram I.

REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CAPPELIO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTICH High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER. US/0 FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS. double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
398 AGSASATCSAAGACSTSSASTITCCCASSAAGCACTSACTSSGAACTTCSCTSAGSAGA 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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RESULT 2
US 08-804-227C-7
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                                                                                                                                        INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kuhstoss, Stuart A. APPLICANT: Rosteck, Paul R., Jr. APPLICANT: Sutton, Kimberly L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 AGGTGÖĞÜÜTÜĞANÜNGANTIĞITINDAN VANATITINDIN GÖLGÖĞÜĞÜĞĞĞĞĞĞĞĞĞĞĞ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 TGGTCCGCCTGGGCTTACGCGCGCTGGGAGACGTCGTGACTCTGCAGGAGAGAGGCTGGAG 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 COGGO ASTROLOS ON TO MACOUS TROUTCOMO COSTO CIDOCO GARCOTO CAGACO COGO 431
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                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
NAME/KET CDS
                                                                          STRANDEDNESS:
                                                                                                                                                                                                                       REFERENCE/DOCKET NIMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46285
                                                                                           nucleic acid
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                                                           linear
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                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08804198 Patent No. 5945320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31225 AGCAGCGCCGACGACGACGACGTTTCGCCTTTCACCGACGA 31265
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APPLICANT:
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                                                                        OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                  ZIP: 46285
COMPUTER READABLE FORM:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE.
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | S08 | GCCATCCGCTGCGTGCGCTCCCCGGGGAGTTCCTGGAACTTCCTCACGCCACGCCACGACAGACTG_ 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARR CTGGACGCCATGGTCTGGCCTACGCGTGGGCAAGGA 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 GGAGAGAGGGCCСТĞÇAĞCGCСТӨГАĞĞСССБАҚАНАЙСАТСАСТАСТАГГАТБАБЕСТСТҚІ 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 CGCGAGGCTTTCGGCTGCCTGCGGGCCGGCCAGTACCCGCGGCGCCCTGGAGCTGCTGCTG 627
                                   APPLICATION NUMBER: US/08/804,198 FILING DATE:
                                                                                                                                 COMPUTER:
                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 5.9%; Score 56.2; DB 2; Length 44377;
Local Similarity 47 A%; Pred. No. 9 0644;
les 163; Conservative 0; Mismatches 178; Indels 0;
                     CLASSIFICATION:
                                                                                                                                                                                                           COUNTRY.
                                                                                                                                                                                                                                                              ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPOPATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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Kuhstoss, Stuart A.
Rao, Nagaraja P
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                                                                                                                                                                                                               Sequence 1, Application US/08209747
Patent No. 5733771
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 163;
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PEGISTRATION NUMBEP: 36,470
PEFERENCE/DOCKET NUMBER: P9:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                NUMBER OF SEQUENCES: 5
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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Best Local Similarity
                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
                                   APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAs Encoding
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
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                                                                                                                                                                                                                                                                                          2162 GSATACGSTGCCGGAGCÁGGAGCTGCTGCAGCTGCTGGAGCAGCAGGAG 2207
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                      COPPESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                              2102 GCAĞĞAĞCTĞĞAĞCTĞĞTĞĞAĞĞTRATTĞĞAĞĞARŞAĞİTİRĞARAİNTARIĞĞTĞĞTĞANĞĞT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 GGCCGGCCAGTACCCGTGGGAGCTGTTGCTGCTGCTGCTGCTGCTGCAGGAGAA 650
                                                                                                                                                                                                                                                                                                                                  831 CTACGCGCTGGGCAAGGACTTCGTGACTCTGCAGGAGAGGCTGGAG 876
                                                                                                                                                                                                                                                                                                                                                                                                                   771 GCAGGCCCGGGGAGGGCCATCGCTACTATGCGCCTCTGCTGGACGCCATGGTCCGCCTGGC 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 183..2675
CTHER INFORMATION: /product= "N. clavipes:
OTHER INFORMATION: ampullate silk protein"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 14-MA
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REFERENCE/DOCKET NUMBER: 1447-104P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
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                                                                           cDNAs Encoding Minor Ampullate Spider
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Sequence 5, Application US/08680506C Parent No. 6008013 ; GENERAL INFORMATION. ; AFFLICANT: Reymolds, Paul R.
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APPLICANT: Reynolds, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO. 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         2162 GRATAGRATIGOGRAFAGRAGAGAGGTTGCTGCAGGTTGCTGGAGGAGGAGGAG
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205 8600
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                      1982 GGAGGCTACGGTGGTGAGCTGAGATAGATACGGTGCCGAGCAGGAGCTGGTGCTGCTGCAGCT 2041
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                              2042 SOTGGTG AFRIATE ESSAGGESETE STESSTTAÐBGTASA SSTGETGGTGGTAGAÐČEGSET. ELDI
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PRIOR APPLICATION DATA:
                                                                                                                                                                                   831 CTACGCGCTGGGCAAGGACTTCGTGACTCTGCAGGAGAGGCTGGAG 876
                                                                                                                                                                                                                                                                                                                                                                                                      771 GCAGGCCCGGGAGGGCCATCGCTACTATGCGCCTTCTGCTGGACGCCATGGTCGCCTGGC 830
                                                                                                                                                                                                                                                                                                                                 711 COGCGACCTCGACCGCCGACGGCCTAGAGCTTTCGGCGAGGGAGAGAGGGCTCGCGCTC770
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hes 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes r
OTHER INFORMATION: ampullate silk protein"
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STATE: Virginia
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 55.6; DB 1; Length 2793; 49 7%; Pred No 0.0039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 1347
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LENGTH: 954
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                                                                                                                                                                                                                                                                                        Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/680,506C
OTEPSENT FILING DATE: 1996-97-98
EARLIER APPLICATION NUMBER: 60/021,672
EARLIEP FILING DATE: 1996-97-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reynolds, Paul R. TITLE OF INVENTION: CHONDROCYTE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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SOFTWARE. Patentin Ver. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                   OKGANISM: Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
714 - G$A***T**G$A**G$C$C$C$A*$A**A***T***T***A*$A$A$A$A$A***C***P$A*A**C$C$199A 773
                                                                             594 СОГОСАВТАССОВОВОССТИВАЮ ГРЭПТИСТВОВ ВТОСТОСОВ ГРЭСАВЗАВАВАЕТ 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 - Фапулоразмазаўскаторстастатаў аўстотаста замором тэрто за староста взз
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                                                                                                                                654 QACCGCCCACTGCCCTGCGGCGGCGGTCCGGGGCCT4TV4C4TGC4TGCTGCTGTGCCACCG 713
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                                                                                                                                                                                                                                                                                Match 5.8%; Score 55.4; DB 3; Length 1347; Local Similarity 49.2%, Fred. No. 0.0038; es 146; Conservative 0; Mismatches 151; Indels 0; Gaps
                                                                                                                                                                                   COMPANTAAGTOLOGOTALISAGSÁGSTISAAGOOGCAOLTÍNGOGGAGGACOOGCTISTOCCT 134
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US-08-680-506-4
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; ORGANISM: Gallus gallus
US-08-680-506-6
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CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
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CURRENT FILING DATE: 1996-07-08
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TITLE OF INVENTION: CHONDROCYTE PROTEINS
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APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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Best Local Similarity 47 2%; Pred. No. 0.0068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/232,468A CURRENT FILING DATE: 1999-01-05 NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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NAME/KEY: CDS
LOCATION: (1)..(2742)
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRAFI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                   STREET: 4 Embarcade
CITY: San Francisco
                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                 COUNTRY: USA
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SOFTWARE:
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VENTION: POLYMOGLECTIDE VACCINE FORMULA AGAINST POPCINE
                                                                                                                                                                                                                                                                                                                                    4 Embarçadero Center, Suite 3400
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                     FLEHR, HOHRACH, TEST, ALBRITTON & HERBERT
                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                    ,SEQ ID NO.
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    Matches 165;
                                           Query Match 5.6%; Score 52.8; DB 6; Length 4897; Best Local Similarity 46.9%; Pred No 0.016;
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TELEFAX: (415) 494-8771
TELEX, 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION NAME: ROWLAND, Bertram REGISTRATION NUMBER. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCHREURS, CHRISTA S ,METTENLEITER, THOMAS N, APTUP J.; LUKAS, NOEMI, RZIHA, HANNS J.
TITLE OF INVENTION: PSEUDORABIES VIRUS VACCINE
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Local Similarity 48.4%;
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                                                                                                                                                                                                                                                                                           FILING DATE: 21-JUL-1989
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                                                                                                                                                                                                                 LENGTH: 4897
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TYPE: nucleic acid
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    Conservative
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APPLICANT: OPPERMANN, HERMJ
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, 1
                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 ACCTOSACCOSCOSOGAGGCCTTCGCGGGCGGAGAGAGGGCCCTGCAGCGCCTGCAGG 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MEYERS, THOMAS C. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
LOCATION: 1..884
OTHER INFORMATION: /note= "hOP-2 genomic sequence"
                                                                                                  NAME/KEY: misc_feature LOCATION: 1..884
                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/901,200A
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SOFTWARE: Patentin Release #1.0,
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                         FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C.
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/901,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CTHER INFORMATION:
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ZIP: 01748
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TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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(508) 435-9001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note: "EXON ONE"
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Pred. No. 0.016;
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INFORMATION FOR SED ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.5%; Score 52.2; DB 3; Length 884; Hest Local Similarity 48.8%; Pred. No. 0.016; Matches 141; Conservative 0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                          09 219-391-11
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LOCATION: 1..837
OTHER INFORMATION: /note= "EXON ONE"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "hOP-2 genomic sequence" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                    NAME/REY: misc_feature
ILOCATION: 884
OTHER INFORMATION: /note= "A GAP OCCURS BETWEEN
OTHER INFORMATION: POSTIONS 884 IN THIS SEQUENCE AND POSITION 1 IN SEQ ID NO 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..884
                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Database: PIR 73:* 1: pir1.* 2: pir2.* 3: pir3:* 4: pir4:*	Post-processing. Minimum Match 10% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 283224	Searched: 283224 seqs, 96134422 residues	Scoring table: RLOSUM62 Gapop 10.0 , Gapext 0.5	Title: US-09-816-697A-2 Perfect score: 1650 Sequence: 1 MASPEHPGSPGCMGPITQCT PPPTPPGITLKELTVREYLH 316	Run on: April 20, 2063, 14:02:01, Search time 45 Seconds (without alignments) 675.077 Million cell updates/sec	OM protein - protein search, using sw model	GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
						VREYLH 316	nds } l updates/sec		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

hypothetical structural protein - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999
C;Accession: T41077
R;McDougall, R.C.; Rajandream, M.A.; Harrell, B.G.; Zimmermann, W.; Wambutt, R. submitted to the EMBL Data Library, August 1999
A;Reference number: Z21822
A;Accession: T41077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1010 <MCD>
A;Residues: 1-1010 <MCD>
A;Cross references. EMBL.AL109357, FIEN.CAB53076.1; GSFEB.GNudues, SFEB.SFCC16A11.04

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	
88.5	88.5	89	89	89.5	90	90	90	90.5	90.5	90.5	90.5	91	91	91	91.5
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T30288	F86286	A39638	D83454	S13512	EDBEIF	A45344	B70374	F75583	D70708	H72670	T40731	729420	S67656	D75197	966675
pristinamycin I sy	hypothetical prote	plectin · rat	conserved hypothet	retinoic acid rece	immediate-early pr	immediate-early pr	conserved hypothe	GGDEF family prote	probable purB prot	hypothetical prote	probable golgi mem	probable transcrip	hypothetical prote	tRNA nucleotidyltı	nypothetical prote

### ALIGNMENTS

hypoth C;Spec C;Date C;Acce R;Lin, M; Ko	B84534  hypothetical protein At2g15900 [imported] - Arabidopsis thaliana  C;Species: Arabidopsis thaliana (mouse-ear cress)  C;Species: Arabidopsis thaliana (mouse-ear cress)  C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02 Feb 2001  C;Accession: B84534  R;Koo, H; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Benito, M.I; Town, C.D.; Fujii, C.Y.  B;Koo, H; Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanaken, S.E.; Umayam, L.; Tallon,  B;Koo, H; Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanaken, G.I.; Tallon,  B;Koo, H;Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanaken, G.I.; C.Y.  Buss D. Mischan M.C. White O. Fisch Th. Callbox G.I.; C.Y.
Natur A;Tit	Nature 402, 761-768, 1999  Nature 402, 761-768, 1999  A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  A;Reference number: A84422; MJID:20083487; FMID:10617197
A;Sta A;Mol	A;Status: ForeIminary A;Status: ForeIminary A;Molecule type: DNA A:Molecule type: DNA A:Mostdines: 1,950 - KSTO
A; Cro C; Gen A; Gen A; Map	A;Cross·references. GB.AE002093; HID.g5306243, FIDN.AAD41976.1, GSFDB.GM00139 C;Genetics: A;Gene: At2g15900 A;Map position: 2
Que Bes Mat	Query Match 7.1%; Score 117; DB 2; Length 952; Best Local Similarity 26.3%; Pred. No. 0.25; Matches 41; Conservative 25; Mismatches 70; Indels 20; Gaps 5;
상	42 HLDTHSGLSSNSSMTTRELOQYWQNQKCPWWHVKLLFEIASARIEERKVSKFVVYQIIVI 101 
Q	102 QTGSFDNHKAVLERFYSDFAKLQKALLKTFFEEIEDVEFPPFHUTGNFAREMIGERP- 158
Db	554 DVENKTWEVKRRYSNEERLHRQLKBIPNYNLQLPEKPIESSSTEIRAFVHRPC 605
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DЬ	159 RALQEYUSLLYAIRCVERSREELDELTRPELREAFG 194

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A;Molecule type: mRNA
A;Residues: 1-473 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 29-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Remarkable homology among the internal repeats of erythroid and nonerythroid sp
A;Reference number: I50420; MUID:85298223, PMID:3862389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P;Birkenmeier, C.S.; Bodine, D.M.; Pepasky, E.A., Helfman, D.M., Hughes, S.H., Burker, Proc. Natl. Acad. Sci. U.S.A. 82, 5671-5675, 1985
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related to MDM1 protein [imported] - Neurospora crassa
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                                                                                                                                                                                                      282 KDFVTLQERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 KKNNHHVENTTAKMKGLKGKVSDLEKANAQRKAKLDE.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 NVEEEEAWINEKMTLVASEDYGDTLAATQGLLKKHEAFETDFTVHKDRVNDVCANGEDLI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 PATGGYLDTGKKLSTONTIGKEETGGKLAPFYDHWKELKQLAAARGQRLEESLEYQQFVA 202
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                                                                                                                                                                                                                                                         AAKHIOSKAIEVRHASLMKPWNQLLANSAAPKKKLLEAGEHERKVECLELTFAKKASAEN 429
                                                                                                                                                                                                                                                                                                                                                                       ADVVESWIGEKENSLKTODYGPOLSSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLL
                                                                                                                                                                                                                                                                                                                                                                                                                            PELREAF----AAVPALCAVLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIRCVRRSREFLDFLTRPELR -- EAFGCLEAG-QYPRALELL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTEREEIEDVEEPRKHLTGNEA--EEMICEPPRALQEYLGLLYAIRCVPRSPEFLDELTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                 -- HRDLDRPAEAFAAGERALQR--LQAREGHRYYAPLLDAMVRLAYALG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 7%; Score 111; DR 2; Length 473
21.2%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128

    chicken (fragment)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches 134; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ... NSAFLQFNWK 309
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C:Accession: T49735
R.Schulte, U., Algn, V., Hobelsel, J., Brandt, F., Fo
submitted to the Protein Sequence Database, May 2000
A.Reference number: 225022
A:Accession: T49735
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C;Species: Neurospora crassa
C;Date: OC Jun 2000 #sequence_revision OC Jun 2000 #Fext_change OC Jun 2000
                                                                F,889-973/Domain: spectrin/dystrophin repeat F;974-1021/Domain: SH3 homology <SH3>
                                                                                                                                                                                                  F;360-465/Domain: spectrin/dystrophin repeat homology <SP4>
F;466-571/Domain: spectrin/dystrophin repeat homology <SP5>
F;572-676/Domain: spectrin/dystrophin repeat homology <SP6>
                                                                                                                                                                                                                                                                                                                                                                   A;Note: residues 1880-2359 are shown between residues 1399 and 1400 in Fig. 2 C;Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/cC;Keywords, actin binding; calcium binding; cytoskeleton; duplication; EF hand; heterodin F;43-17/Domain. spectrin/dystrophin repeat homology <SP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type. mRNA
A;Residues: 1-2477 <WA2>
A;Cross-references: EMBL:X13701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Primary structure of the brain alpha-spectrin. A, Reference number. A31866; MUID:89093238, FMID:2910879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P;Wasenius, V.M.; Saraste, M.;
J. Cell Biol. 108, 79-93, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type. mRNA
A; Residues: 1-2477 < WAS >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Aug 1997 ()Accession. A3:122, A3:1866, A2:2733, S9:2425, S0:120 R;Wasenius, V.M.; Saraste, M.; Salven, P.; Eraemaa, M.; Holm, L., Lehto, V.: J. Cell Biol. 108, 1177-1178, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: calspectin alpha chain; fodiin alpha chain C; Species: Gallus gallus (chicken)
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A;Residues: 1-1104 <SCH>
A;Residues: 1-1104 <SCH>
A;Residues: 1-109 <SCH-
A;Ropes:meferences. EMBL.AL356192, GSFDB GNC0116, NGSF BC4B19 70
A;Experimental source: BAC clone B24B19; strain OR74A
                                                                                                                                    F;677-782/Domain: spectrin/dystrophin repeat F;783-888/Domain: spectrin/dystrophin repeat
                                                                                                                                                                                                                                                                                                                                              F;148 253/Domain: spectrin/dystrophin repeat homology <SF2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A31866
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,1090 1231/Domain: spectrin/dystrophin repeat homology #status atypical <SP10>
,1232 1337/Domain. spectrin/dystrophin repeat homology <SP11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                             254 359/Domain. spectrin/dystrophin repeat homology <SP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    850 EKYLNOLLLEDVCHSRELRTFLSQ 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 QEYLGLLYAIRCVPRSPEFLDFLTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 GSFDNNKA--VLERRYSDFAKLQKALLKTFREETEDVEFPRKHLTGNFAEEMICERERAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 SKASLQRETRRKELQRQQYVTQESDNSLYGRSTIKTKNIHVGREFDGKEFAMYATEVLRN 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 SGLSSNSSMTTREL--COYMONOKOPWKHVKLLFEIASARI-EERKVSKFVVYOIIVIOT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
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25.5%, Pred. No. 0.9,
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                                                                                                 homology
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                                                                                                                                                                        <SP7>
                                                                                                    #status atypical <SP9>
                                                                                                                                        <SP8>
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A;Title: Nuclear and mitochondrial inheritance in yeast depends on novel cytoplasmic st A;Peference number: A4263C; MUID:92332595; PMID:1378448
A;Recession: A4263C MUID:92332595; PMID:1378448
A;Recession: A4263C MUID:92332595; PMID:1378448
A;Recession: A4263C MUID:92332595; PMID:1378448
A;Residues: 685-771; /P', 773-898, /I', 900-1062, /K', 1064:1080, /S', 1082:1095, /R', 1097-1127
A;Gross-references: EMBL:XF6371; NID:9391E, PIDH:CAA47014.1, FII:33376
A;Gross-references: EMBL:XF6371; NID:9391E, PIDH:CAA47014.1, FII:33716
A;More: sequence extracted from NCBI backbone (NCBIN:108433, NCBIF:108434)
R;Stirling, C.J.
submitted to the EMBL Data Library, February 1995
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F;2328-2360/Domain:
F;2371-2403/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDM1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein 0 13; protein YM8339
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
S47445
                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z49210; MIFS.YMU104c
R;McConnell, S.J.; Yaffe, M.P.
J. Cell Biol. 118, 385-95, 1992
                                                                                                                                                                                                                                                                                                                                                                                                R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: $53954
A;Accession: $53968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-676 < BAR >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Barrell, B.G. submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revisi
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                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 673-1127 <SKE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X80835; NID:g530339; PID:g530340; MIPS:YML104c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S47445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDFVTLQERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAKHIQSKAIEVRHASUMKRWNQLLANSAARKKKLLEAQEHFRKVEDUFUTFAKKASAFN 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADVVESWIGEKENSÜKTDDYGPDLSSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELREAE-----GCLEAGQYPRALELLLRVLPLQEKLTAHCPA------AAVPALCAVLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKNNHHVENITAKMKGLKGKVSDLEKAAAQRKAKLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAIQGVLDTGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQRLEESLEYQQFVA 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGPDGHLDTHSGLSSNSSMTTPELOOYWONOKCPWKHVKLLFEIASAPIEEP-KVSKFV- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTEREEIEDVEEPPKHLTGNEA--EEMICEPPRALQEYLGLLYAIPCVPPSPEFLDELTR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S47445; S53968; A42636; S51916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEDIDPPAEAFAAGEPALOP--LOAPEGHPYYAPLIDAMVELAYALG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein YM8339 15c; protein YML104c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 111;
Fred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology <SP15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NSAFLQFNWK 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology <SP20>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology <SP17>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology <SP16>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology <SP14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <SP12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <SP19>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <SP18>
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A; Molecule type: mRNA
A; Residues: 1-030 < HON's
A; Cross-references: GB: Z44828, NID g243613, PIDH-AAA46774 1, PID:
A; Cross-references: GB: Z44828, NID g243613, PIDH-AAA46774 1, PID:
A; Cross-references: GB: Z44828, NID g243613, PIDH-AAA46774 1, PID:
C; Superfamily: spectrin/dystrophin calmodulin repeat homology <SP12>
F; 799-904/Domain: spectrin/dystrophin repeat homology <SP19>
F; 799-904/Domain: spectrin/dystrophin repeat homology <SP19>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spectrin alpha chain, nonerythroid - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 21 May-1990 #text_change 29-Sep-1999
C;Accession: A32612
R;Hong, W.; Doyle, D.
J. Biol. Chem. 264, 12758-12764, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 264, 12758-12764, 1989
A;Title: Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.
A;Reference number: A32612; MUID.89327227; FMID.2753883
A;Accession: A32612
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A;Cross·references.
A;Map position: 13L
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A;Accession: S51916
A;Molecule type: DNA
A;Residues: 874·1127 <STI>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;913-1019/Domain: spectrin/dystrophin repeat homology <SP20>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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129
                                                                                                                                                                                                                                                    587 NVEEEEAWINEKMILVASEDYGDILAAIQGLLKKHLAFETDFTVHKDRVNDVCTNGQULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     896 RFLTDP 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 DFLTRP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                      37 PGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCRWKHVKLLFEIASAPIEEP-KVSKFV- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDLMPQLQDL-FPSKVKMSLKYHVTKTLLYE---EPKQKLEYYLPELLSISEICEDNIFP
                                                                   ADVVESWIGEKENSIKTOFYGFÐÍSSVOTLÍTKÓETFÐÁGLQÁFOÐEGIÁNITKÍKÐÐÍÍ
                                                                                                              PELREAF-----GCLRAGOYPRALELLLRVLPLOEKLTAHCPA-----AAVPALCAVLL
                                                                                                                                                              KKNNHHEENISSKMKGINGKVSDLEKAAAQPKAKLDE------NSAFLQFNWK
                                                                                                                                                                                                       KTPPREIEDVEFPPKHLTGNFA--EEMICEPPPALCEYLGILYAIPCVPPSPEFLDFLTR 186
                                                                                                                                                                                                                                                                                                                                           PAIQGVLDTGKKLSDDNTIGQEETĞĞRLAQFVEHWKELKQLAAAPGQFLEESLEYÇQFVA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PE---EIEDVEFFFK-----HUTGNEAEEMICEFFFALGEYLGLLYAIRCVERSREFL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENSSNGLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EIASARIEERKVSKFVVYQIIVI-----QTGSFDNNKAVLERRYSDFAKLQKALLKTF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLILKADITMNOMOLKITAKSORTLIKELEMKELLKÖÖYMVOENGNSIFRKIKIKISKSKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:X65783, NID.g671637, PID.g671638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- ITYYIINIHHFNNGQVSSWD----MARRYNEFFELNTYLKKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.4%;
                                                                                                                                                                                                                                                                                                  -----VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; Score 102; DB
20.4%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 1030;
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PGAY; SH3 homology; spectrin/
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                                                                     753
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A;Title: The structure of the human synapsin I gene and protein
A;Reference number: A35363; MUID:90243651; PMID:2110562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 01-Dec C;Accession: A35363; B35363; A35805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
T14790
A;Accession: B35363
A;Status: proliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          글
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A;Molocule type: mRNA
A;Residues: 1 1325 <BLU>
A;Cross-references: EMBL,AL110273
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(;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 09 Jun 2000
(;Arcussion: T14790
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A; Residues: 1-705 < SUE>
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                                                                                                                                                                       A;Cross-references: GB:M58371; GB:J05431
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6.1%; Score 101; DB 2; Length 1325;
Local Similarity 20.8%, Pred No. 7 1;
nes 65; Conservative 43; Mismatches 136; Indels 6
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A,Residues: 1 659,'KASPAQAQP' <5U2>
A;Cross-references: GB:M58378; GB:J05431
A;Cross-references: GB:M58378; GB:J05431
A;Saurtwald, A, Hoesche, C, Oschwald, F., Kilimann, M.W.
J Biol Chem 265, 14932-14937, 1990
A;Title: The K:-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-less,
A;Peference number: A35805; MUID:90368667; PMID:2118519
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A;Residues: 1-475 <-LET>
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A;Title: Comparison of nonerythroid alpha spectrin genes reveals strict hemology among di
A;Reference number: A93097; MUID-88094373; PMID-3336352
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C;Date: 19 May 1989 #sequence_revision 19 May-1989 #text_change 29-Sep-1999
C;Accession: A27671
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C;Species: Rattus norvegious (November 1971)
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A;Map position: Xpll 23-Xpll.23
C;Keywords: actin binding; alternative splicing; phosphoprotein
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A; Residues: 1-125 < SAU >
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Local Similarity 25.0%;
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Local Similarity 20.4%;
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                                                                                                        94 V-----VYQIIVIQTGSFUNNKAVLERRYSDFAKLQKA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T.L.; Fortugno-Erikson, D ; Harton, D ; Yang-Feng, T L ; Francke, H ; Harris, A (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGLLYAIRCVRRSREELDE-LTREELERAPGCLPAGGYPRALELLLRVLFLGEKLTAHCD 223
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VANVEEEEAWINEKMTI.VASEDYGDTLAAIQGLLKKHEAFETDETVHKDEVNDVCTNGQD 165
                                                                                                                                                                                                                                                                                                                                PHPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCPWKHVKLLFEIASAPIEEP-KVSKF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPPGAHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSLSNAVKQTT--- 88
                                                                                                                                                                                                                 PEQAIQGVLDSGKKLIDDNTIGPEEIQQPPEQEVEHWKELKQLAAARGQPLEESLEYQQE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                               64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               47, Mismatches 135,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indeis
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A,Molecule type: mRNA
A,Residues: 'R',1595-1610,'E',1612-1614,'P',1616-1624,'S',1626-1638,'P',1640,'E',1642-16
2-1813,'R',1815-1820,'K',1822-1844,'V',1846-1850 <MUT>
A,Note. the sequence in Fig. 4 is inconsistent with the sequence in Fig. 3 at several po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M24773; NID-q537330; PIDN-AAA52468.1; PID:q537331
R;Mutha, S.; Langston, A.; Bonifas, J.M.; Epstein Jr., E.H.
J. Invest. Dermatol. 97, 383-388, 1991
A;Title: Biochemical identification of alpha-fodrin and protein 4.1 in human keratinocyt
A;Reference number: A61369; MHID:91341201; PMID:1875039
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A;Molecule type: mRNA
A;Residues: 1-2472 «MOO»
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                                                                                                                                            R:Lundberg, S.; Bjoerk, J.; Loefvenberg, L.; Backmann, L. submitted to the EMBL Data Library, May 1995
A;Description: Cloning and characterization of two putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Structure and evolution of a non-erythroid spectrin, human alpha-fodrin A;Reference number: ISD382; MUID:88093942; FMID:3691949
A;Accession: ISD382
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                                                        A;Reference number: S54877
A;Accession: S54877
                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 811-1299, 'I', 1301-1529 < MOR>
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A;Accession: G01810
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A; Residues: 676-1594, 'P' < PES >
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Biochem. Soc. Trans. 15, 804-807, 1987
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A;Status: preliminary
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A/Title: Generation of diversity in nonerythroid spectrins Multiple polypeptides are
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                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:U26396; NID.g836668, FIDN:AAB60364.1, PID.g836669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 LLCHRDLDRPA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLAAKHIQSKAIEARHASLMKPWTQLFANSATPKKKLLEAQSHFRKVEDLFLAFAKKASA
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                                                                                                                                                  calcium-binding
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hypothetical protein Y50E8A.d - Caenorhabditis elegans
C;Spaceies: Caenorhabditis elegans
C;Date: 29 Oct.1999 #sequence_revision 29-0at-1999 #text_change 29-0at-1999
A;Experimental source: clone Y50E8AC;Genetics:
                                                                                                                                                                      submitted to the EMBL Data A; Reference number: Z21047 A; Accession: T31608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;572-676/Domain: spectrin/dystrophin repeat homology <SP6>F;677-782/Domain: spectrin/dystrophin repeat homology <SP7>F;974-1021/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lundberg, S.; Bjoerk, J.; Loefvenberg, L.; Backman, Eur. J. Biochem. 230, 658-665, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 2059-2312,'F',2314-2346,'EF',2349-2433 <LUN>
A;Cross-references: EMBL:X86901
                                                          A; Cross-references. EMBL: AL117200,
                                                                                A; Molecule type: DNA
A; Residues: 1-459 <WIL>
                                                                                                                                                                                                                                                                  R;Steward
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C;Keywords; actin binding; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 2320-2346, 'EF', 2349-2406 <LU2>
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                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                           C;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1992 IGEKENSLKTDDYGRDLSSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLLAAKHVQS 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1935 DLIKKN----NHHEENISSKMKGINGKVSDLEKAAAQRKANVDENSAFLQFNWKADVVESW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1878 N---VEEEEAWINEMMTLVASEDYGDTLAAIQGLLEEGHEAFETAFTVIIKDEVNOVGTNGQ 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2052 KATEAPHASLMKFWSQLLANSAAPKKKLLEAQSHFRKVEDLFLTFAKKASAFNSWFENAE 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 ERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 PGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCFWKHVKLLFEIASARIEER-KVSKFVV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDB:SPTAN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HRDLDRPABAFAAGERALQR--LQAREGHRYYAPILDAMVPLAYALGKDFVTLQ
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Pred. No. 22;
                                                    NID:e1549770; PIDN:CAR55047.1; CESP:Y50E8A.d
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R;Liu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G. Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996
A;Title: Human plectin: organization of the gene, sequence analysis, and chromosome local A;Reference number: Cc9404; MUID-96216632, PMID 8633055
A;Accession: C59404
A;Status: preliminary
                                                                                                                                                                                          C;Sprcies: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C;Accession: C59404; A59404
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C;Date: 11.Jun-1999 #sequence_revision 11-Jun-1999 #rext_change 13-Aug-1999
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A;Cross-references: EMBL-AL049989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp564F052 1 human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                      194 LLSKTGOTVRAVASSMR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 CL RAGOYPRALELLLR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 IVEGIVERFHORFISTERKALHEFIHRIARHETITENERFEILTAQAWELSCHEKQGPG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 PRKHLTGNFAEEMICERRRALQEYLGILIYAIRCVRRSREFI.DFLTRP--EL----REAFG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 CAVILCHPOIDPPAEAFAAGERALQRIQAREGHRYYAPLIDAMVR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 CVRRSPEFI.DFLTPPE--I.PEAFGCLPAGQYPRALELLLRVLPLQEKLTAHCPAAAVPAL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 DIYTEPTDDETVSTTNEEMNESVPFAVV - GSIDFVEKENGQMVFARQYFWGIVEVEN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 PTGH-----GLKALDLYTLRELAKRYNVIPVIAKSDTTCKDELLRFK-AKILSELKSQKI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 LAQKHPEHQDEFSRRELTLREEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 ESHCDFVKLREALLRTNVDEMRQ----RTHESLYENYRRDRLRQMKIGDGE-TGPKIIEK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match
5.9%; Score 97.5; DI
Local Similarity 28.5%; Pred No 3.4;
nes 39; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 PDGHLDTHSGLSSNSSMTTRELQQ------YWQNQKCRWKHVKLLFEIASARI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 IETFITYRIITKTSRGEFDSSEFEVRRRYQDFLWLKGKLEEAHPTLIIPPLPE-----KF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 VSKEVVYQIIV-IQTGSFENNKAVLERRYSDF-- AKLQKA----LLKTEREEIEDVEF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDFAKLOKALLKTSPESIEDVEFPRKH--LTGNFASEMICEPPPALCEYLGLLYAIP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VTEGDMRKVEEGLAARER----EVHENYNREASKLDMEIR 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 77; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
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conserved hypothetical protein PA2613 [imported] - Fseudomonas acruginosa (strain PAO1) C;Species: Pseudomonas acruginosa C;Species: Pseudomonas acruginosa C;Species: 15:Sep.2000 #sequence_revision 15 Sep.2000 #text_charge 31-Dec 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-4684 <STO>
A;Cross references: GB.CAA91196, HID:g1296662, FIDH.CAA91196.1
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein Si
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A;Peference number: ARC950; MUID:20437337, FMID:10984043
A;Accession: C83318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: C83318
P;Stover, C.K.; Fham, X.Q., Erwin, A.L., Mizeguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y., Broly, L.; Coulter, S.F., Felger, F.F.; Kar, A., Larbig, M.J.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A; Residues: 1-441 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Haemophilus influenzae conserved hypothetical protein HI1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: PA2613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 LDAMVRLAYALGKDFVTLQERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 HPGLHOSTEFFOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 HRDLDPPAEAFAAGEPALQPLQAPEGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635 APATQVAQVTLQSVQRRPELEDSTLRYLQDLLAMVEENQHPVDGAEWGVDLPSVEAQLGS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 CPAMAV ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575 VERDLDKADSMIPILFNDVQTLKNGRHÞQGSGQMYPÞVYÞÍHEÞÍVAÍÞTEYNI.ÞI.KAGVA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 FLDFLTRPE--LREAFG---CLRAGQYPRALELLLRVLPLQEKLTA------H 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 LEPEKOLPSEFEPLECTOPIVTKLOMEAGLCEEQLHQADALLOSDIFILAAGKVPOFAGE 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 L---KTERBEIEDVEFPRKHLTINFAEEMICERR----RALDEYLJJLLYAIRCVERSKE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 WSQFLEFEEMELPAKEADKNRSKGIYQSLEGAVQAGQLKVPFGYHPLDVEKEWGKLHVAI 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 FVQDGVPAN-----ELQLPWQEYP ELVLLLQWMPHHTAAFEEPRFPSSFEEIEIL 454
                                                                    128 VERGTUIFIGATTENESFELNWALLSFAFVYVLKGLLEAALSFLVGKALNEDFGGGFFFL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 -SKFVVYQIIVIQTGSFDNNKA-----VLEPPY-----------SDFAKLQKAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 DAHFETISAVLSG----VKEIRQAVEVAKQHAAQYGRFTILFVDEVHRFNKSQQDAFLPY 127
                                                                                                                                                                                                                                                                       40 DGHLDTHSGLSSNSSMTTRELQQYWQNQK---CPWKHVKLLFEIASAPIEEPKVSKFVVY 96
                                                                                                                                                                                                                                                                                                                                                                             Match 5.8%; Score 96; DB 2; Length 441; Local Similarity 21.4%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 97; DB 2; Length 4684; Local Similarity 20.3%; Pred. No. 69; Local Similarity 20.3%; Pred. No. 69; Indels 146; Local Similarity 51; Mismatches 109; Indels 146;
                                                                                                                                  INIIO
                                                                                                                                                                                                                                                                                                                                            Conservative 47; Mismatches 132; Indels 114;
                                                                                                                                     <u>CTGSFDNNKAVLER</u> RYSDFAKLQKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIEPARSDEGOLSPATPGAYPDCLGPLDLOYAYILMSSYAPIRS 751
-----LKTFREEIEDVEFPRKHLTGNFAEEMICERRR-----A 160
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203 PALELILPVI.PLQEKITAHCPAAAVPAI.CAVLICHPDI.DPAEAFAAGEPALQBLQAPEG 262 302 RALGELLSAWDVQERLGSPEGELAVAQAIVYLACAPKSNAVYSAFAAGEPALQBLQAPEG 262 302 RALGELLSAWDVQERLGSPEGELAVAQAIVYLACAPKSNAVYSAFAAAMRDVAESGGRE-360 263 HPYYAPLLDAMVPL			# H	D
248 FYDUISALHKSVKGSNPDAALYWFARMLDGGCDPLYIARRVVRMASEEVG 203 PALELLLPVL.PLQEKLTAHCPAAAVPAI.CAVLLCHPDLDRPAEAFAAGEPALQELG	SLKIRDKLEHL 427	ง. ฏ-	n -	1
248 FYDUISALHKSVKGSNPDAALYMFARMLDGGCDPLYIARRVVRMASEEVG 203 PALELLLPVI.PLQEKLTAHCPAAAVPAI.CAVLLCHBDLDRPAEAFAAGERALQELG		- GI	303	Ş
248 FYDUISALHKSVKGSNPDAALYWFARMLDGGCDPLYIARRVVRMASEEVG 203 PALELLLPVLPLQEKITAHCPAAAVPALCAVLLCHPDLDRPAEAFAAGEPALQELG 203 PALELLLPVLPLQEKITAHCPAAAVPALCAVLLCHPDLDRPAEAFAAGEPALQELG 302 RALGLCLSAWDVQERLGSPEGELAVAQAIVYLACAFKSNAVYSAFNAAMRDVAESG 263 HPYVAPLLDAMVPL	VPLHLRNAPTKLMKSLGYGEEYRYAHDEPDAYAAGEDYFPEDL		361	D
	YAPLLDAMVPLAYALGKEFVTLQEPL	H	262	Š
	JGLCLSAWDVQERLGSPEGELAVAQAIVYLACAPKSNAVYSAFNAAM	70 - 20 -	302	Db
246 FIDUISALHKSVRUSNPDAALYWFARMLDGGCDPLYIARRVVRMASEEVG	JELLLPVI,PLQEKITAHCPAAAVPAI.CAVLLCHRDLDRPAEAFAAGE	ر الا – الا –	203	9
	FYDQISALHKSVRGSNPDAALYWFARMLDGGCDPLYIARRVVRMASEEVGNADP 301	εFY	248	DЪ
161 LQEYLGLLYAIRCVRRSPEFI.DFLTRPELREAFGCLRAGQYP	SYLGLLYAIRCVRRSPEFIDEFITPPELRE	1 10	161	Ş
	>EESFQVLLAAADGDGRRLLNLLENAADLAEDGSEISPELLQNLLGD		186	DЬ

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Deloukas P., Matthews L.H., Ashuret J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A K., Bagguley C L., Builey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J., Boasley O.P., Bird C P., Plakey S E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Burler A P., Garder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C M., Clark G., Conley V.E., Collier P E., Conner P.E., Cotby N R., Coulson A., Coville G.J., Deadman R., Dhami P D., Dunn M.,
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                            MEDLINE-21638749; Pubmed 11780052
                                                                                                                                                                                                                                                                                                                                                                  Stavrides G.S., Huckle E.J., Deloukas P.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A new member (SNX21) of the sorting nexin protein family."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa,
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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SNX21 OP C20OPF161
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PROSITE; PS50195; PX; 1.
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Primates;
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Catarrhini; Hominidae; Homo.
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RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam P., Hall P.E.,
RA Hammond S., Harley J.L., Heath P.D., Holden J.L., Howden P.J.,
RA Hinckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kdy M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lchvastatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Kdy M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Mines S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
RA Milme S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
RA Milme S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
RA Milmer R., Parker A., Patel P., Pearce T.A. V., pack A. I.,
RA Milmore R.J.C.T., Prathalingam S.P., Phimb P.M., Pamsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen P., Sims S.,
RA Swann P.M., Sydamore N., Taylor R., Tee L., Thomas D.M., Thorpe A.,
RA Swann P.M., Sydamore N., Taylor R., Tee L., Thomas D.M., Thorpe A.,
RA Milming J., Wray P.W., Hibbard T., Purbin P.M., Bentley D.R., Beck S.,
RA Norers J., Whittaker P., Willey D.L., Williams S.A.,
RA Milming J., Wray P.W., Hibbard T., Purbin P.M., Bentley D.R., Beck S.,
RA ROCERS J., Whittaker P., Willey D.L., Williams S.A.,
RA ROCERS J., Whittaker P., Willey D.L., Williams S.A.,
RA ROCERS J., Whittaker P., Willey D.L., Williams S.A.,
RA ROCERS J., Whittaker P., Willey D.L., Williams S.A.,
RA ROCERS J., Whittaker P., Willey D.L., Williams S.A.,
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RA ROCERS J., Whittaker P., Willey D.L., Williams S.A.,
RA ROCERS J., W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport; Protein transport.
DOMAIN 129 246
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EMBL; AL008726; CAC36011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the interpopean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 414:865-871(2001)
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SIMILAPITY BELONGS TO THE SOPTING NEXIN FAMILY.
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VREYL 315
                                                LODESTHETTALETERHANDISMEDS
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                                                                                                                                                           TGLYREALALMANAMQUQAQUGTPSGPPDRPLLITLAGLAV(HQELEDPGEAPA)(TEKAUQL
                                                                                                                                                                                                              AGQYPRALELLLRVLPLQEKL-TAHCPAAAVPALCAVLLCHPDLDRPAEAFAAGERALQR
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                                                                                                    <u>LOAREGHRYYAPILLDAMVRLAYALGKDFVTLQERLEESGLRRFTPRGIT</u>
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Q9NRS6; Q9NRS5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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J. Biol Chem. 276:5974-5984(2001).

-!- FUNCTION- MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR TRAFFICKING. OVEREXPRESSION OF SNX15 DISRUPTS THE NORMAL TRAFFICKING OF PROTEINS FROM THE PLASMA MEMBRANE TO RECYCLING TRAFFICKING OF PROTEINS FROM THE PLASMA MEMBRANE TO RECYCLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Protein transport; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001683; PX.
Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:14978; SNX15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF175267; AAF89955.1; -. EMBL; AF175268; AAF89956.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                           194
          246 AFAAGERALQRL---
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ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
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                                                                  ---RGGEVTRPLEVSRDLHILPPPLIPT---PPPDDPRLSQLLPAERRGLEELEVFVDPP
                                                                                                                                                                                                   LEEFPAFPRAQVFGFFEASVIEERPKGAEDLLRFTVHIPALNNS----
                                                                                                                                                                                                                                                                 VE----FPRKHLTGNFAEEMICEPPRALQEYLGLLYAIRCVERSREFLDFLTRPELREAF 193
                                                                                                                                                                                                                                                                                                                                YTVSDPRTHPKGYTEYKVTAOFISKKDPEDVKEVVVWKPYSDFPKLHGDLAYTHPNLFRP
                                                                                                                                GCLRAGQYPRALEIL--LEVLPLQEKLTAHCPAAAVPALCAVLLCHR----DLDRPAE-- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is S.A., Barr V.A., Haft D H., Taylor S I , Haft C P , fication and characterization of snx15, a novel sorting nexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 AA; 38291 MW;
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---QAREGHRYYAPLLDAMVRLAYALGKDFVTLQERLEESQLRRP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 123; DB 1;
24.9%; Pred. No. 0.0055;
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-!- FUNCTION: May be involved in several stages of intracellular trafficking (By similarity).
-!- SIMILAPITY: BELONGS TO THE SOFTING NEXIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport; Protein transport.
DOMAIN 1 125
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SMART; SM00312; FX; 1.
PROSITE; PS50195; PX; 1
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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"SBBI31 as a new member
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192 AFGC 195
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Best Local Similarity
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01-AUG-1991 (Rel. 19, Last sequence update)
16-0CT-2001 (Pel. 40, Last annotation update)
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                             Spectrin alpha chain, brain (Spectrin, (Fodrin alpha chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel member (SNX27) of the sorting nexin family."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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InterPro; IPR000159; PA_domain
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-!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
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OR SPTA2
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                                                        non-erythroid alpha chain)
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Trave G., Lacombe J.-P., Pfuhl M., Saraste M., Pastore A.;
"Molecular mechanism of the calcium-induced conformational change in
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Pascual J., Pfuhl M., Walther D., Saraste M., Nilges M.;
"Solution structure of the spectrin repeat: a left-handed antiparallel triple-helical coiled-coil.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98363217, FubMed=9699637,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Cell Biol. 108:1177-1178(1989)
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Lehto V.-P
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EMBO J. 14.4922-4931(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 359:851-855(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 965-1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 4:1425-1430(1985).
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                                    NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES REPEATS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH OTHER N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT FORM TYPICAL SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MORPHOLOGICALLY, SPECTRIN-LIKE PROTEINS APPEAR TO RELATED TO SPECTRIN, SHOWING A FLEXIBLE POP-LIKE STRUCTURE. THEY CAN BIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULIN-RINGING ACTIVITY. IN NONERYTHEOID TISSUES, SPECTRINS, IN ASSOCIATION WITH SOME OTHER PROTEINS, MAY FLAY AN IMPORTANT
SIMILARITY: BELONGS TO THE SPECTRIN FAMILY SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROLE IN MEMBRANE ORGANIZATION.
SUBUNIT: LIKE EPYTHPOCYTE SPECTRIN,
                                                                                                                                                                                                                  (5) <del>(4</del>)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE
                                                                                                                                                                                                                                                                                                                                                                                                                             TETRAMERS.
                                                                                                                                                                                                                  MIDDLE DOMAIN (M), DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC), C-TERMINAL DOMAIN (C).
                                                                                                                                                                                                                                                                                                                    N-TERMINAL DOMAIN (N), DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE SPECTPIN-LIKE PROTEINS
                                                                                                                                                    TO EACH
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rodom; pD000066; ...;
sMART; SM00054; EFh; 2.
SMART; SM00156; SPEC; 20.
SMART; SM00150; SPEC; 20.
SMART; SM00150; SPEC; 20.
SMOOTTE; PS00018; EF HAND; 2.
PPOSITE; PS50002; SH3; 1.
Cytoskeleton; Membrano; Calmodulin binding; Actin-binding; Cytoskeleton; Calcium-binding; Repeat; SH3 domain; 3D-s
N-Terming protein; Calcium-binding; Repeat; SH3 domain; 3D-s
N-TERMINAL DOMAIN.
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EMBL; X14519; CAA32663.1;
EMBL; X02593; CAB51571.1;
PIR; A30122; SJCHA
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ProDom; PD000012; EF-hand; 1.
ProDom; PD000066; SH3; 1
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Pfam; PF00435; spectrin; 23.
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1TUD; 01-AUG-96
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1AJ3; 07-JUL-97
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                                                                                                                                                                                   C-TERMINAL DOMAIN.
EF-HAND 1 (POTENTIAL)
EF-HAND 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIDDLE DOMAIN.
                                                                                                                                                                                                                               TERMINAL DOMAIN
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RESULT
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Best Local S
Matches 66
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01-00T-1993 (Rel. 27, C
16-00T-2001 (Rel. 40, I
15-JUN-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1883
                                                                                                                                        Submitted (FEB-1995) to the EMBL/GenBank/DDI--!- FUNCTION: Essential for mitotic growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1823
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                                                                                                                                                                                                                  cytoplasmic structures defined by the MDM1 protein."; J. Cell Biol. 118:385-395(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural protein MDM1.
MDM1 OR YML104C OR YM8339.15C.
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            This SWISS-PROT entry is copyright
                                                                                                                                                                                                                                                           MEDLINE=92332595, PubMed_1
McConnell S.J., Yaffe M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDM1_YEAST
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                           "Nuclear and mitochondrial inheritance in yeast depends on
                                                                                                                                                                                                                                                                                        SEQUENCE OF 633-1127 FROM N.A.,
                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                     Walsh S.V
                                                                                                                                                                                                                                                                                                                                                  Devlin K., Skelton J., Churcher C., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=4932;
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                                                SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: TO S.POMBE SPCCIA11.04.
SIMILARITY: CONTAINS 1 PX DOMAIN.
SIMILARITY: CONTAINS 1 PXA DOMAIN.
CANTION: Pef 2 sequence differs from that shown due
                                     frameshift in position 638.
                                                                                                                             inheritance.
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                                                                                                                                                                       OF 874-1127 FROM N.A.
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between the Swiss Institute of Bioinformatics and the

EMBL outstation

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RESULT
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                                                                                                                                                                                                                                           P16086; P70477; O88663;
01-APR-1990 (Rel. 14, Created)
15.JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
(Alpha-II spectrin) (Fodrin alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
SGD;
              Kalamaraki P., Gazzotti P.; "Structural and functional characterization of the calmodulin calpain binding domains of rat liver_alphaII_spectrin.";
                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryora; Meraroa; Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodenria; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02194; PXA; 1. SMART; SM00312; PX; 1. SMART; SM00313; PXA; 1
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                               STRAIN=Wistar; TISSUE=Liver; Kalamaraki P., Gazzotti P.,
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      SPCN RAT
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S0004572; MDM1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z49210; CAAR9114 1; ALT_INIT.
X66371; CAA47014.1; ALT_FRAME
X65783; CAA46664 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00787; PX; 1
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26.3%;
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063 R -> 1
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EMBL; AF084186; AAC33127.1; -.
EMBL; AF084186; AAC33127.1; -.
EMBL, Jn4828, AAA40770.1; -.
FIR, A32612; A32612.
HSSP, P07751, 1AT7
                                                                                                                                                                                                                                                                           Pfam; PF00018; SH3; 1.

Pfam; PF00036; efhand; 2.

Pfam; PF00435; Spectrin; 33.

SMART; SM00054; EFh. 2.

SMART; SM00056; SH3; 1.

SMART; SM00150; SPEC; 29.

PROSITE; PS00018; EF HAND; 2.

PROSITE; PS00002; SH3; 1.
                                                                                                                                                                                                                                              Capping
REPEAT
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                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou D , Ursitti J A , Porter N C , Fandall W P , Rloch R.J.; "Expressional cloning of alpha-fodrin from rat skeletal muscle."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.";
J. Biol Chem 264:12758-12754(1989)
--- FUNOTION: FODPIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1292-2321 FROM N.A.
                                    REPEAT
                                                                                                      REPEAT
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                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                   Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hong W., Doyle D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89327227; PubMed-2753883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                         InterFro; IFR001452;
InterFro, IFR002017;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
SIMILARITY: CONTAINS 1 SHAJ DOMAIN.
SIMILARITY: CONTAINS 23 SPECTPIN PEPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOSKELETON AT THE MEMBRANE (By similarity). SUBUNIT: LIKE EPYTHROCYTE SPECTRIN, THE SPECTPIN-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRAMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE
                                                                                                                                                                                                                                                         protein;
                                                                    1062
1091
1208
1233
1339
  1445
1551
1658
1764
1870
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SH3
                                                                                                                                                                                                                                                                                                                                                                                                 EF-hand
                                                                                                                                                                                                                                                                                                                                                                         Spectrin
                                                                                                                                                                         SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 5.
SPECTRIN 6.
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CA_BIND
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                                                                                                                                                                                                                                                                                Hanson B.J., Hong W.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: May be involved in several stages of intracellular trafficking (By similarity).
Trafficking (By similarity).
SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1985
                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorting nexin 16
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15-JUN-2002 (Pel
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16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-prefit institutions as long as its content is in no way the suppose the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the sup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKNNHHEENISSKMKGLNGKVSDLEKAAAQRKAKLDE
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AF305779; AAG25676.1;
P14598; 1GD5.
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Similarity 20.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40, Last sequence upcare, 41, Last annotation update)
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2321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECTRIN 22.

SPECTRIN 23.

EF-HAND 1 (POTENTIAL).

EF-HAND 2 (POTENTIAL).

D -> Y (IN REF. 1).

V -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 1; Length 2472; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KL -> NV (IN PEF 1).
KL -> NV (IN REF. 1).
QQIQARNTTGVT -> HADPGQEHNPSH (IN PEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08DDF01A2871278A CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 AA
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                                                                                                                   Usage
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                                                                                                                   and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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SPCN
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q13813, Q16696, Q9FOVC, Q13186;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non-er;
(Alpha-II spectrin) (Fodrin alpha chain).
SpTAN1 OR SPTA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transport; Protein transport; Coiled coil.
DOMAIN 105 218 PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1
                                                                                SEQUENCE OF 676-1595 FROM N.A.
MEDLINE=87277023; FubMed=3038643,
McMahon A.P., Glebelhaus D.H., Champion J.E., Bailes J.A., Lacey S.,
Carritt B., Henchman S.K., Moon R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
   McMahon A.P.,
                    ERRATUM
                                         "cDNA cloning, sequencing and chromosome mapping spectrin, human alpha-fodrin."; Differentiation 34:68-78(1987)
                                                                                                                                                                Biochem. Soc.
                                                                                                                                                                                                             McMahon A.P., Moon R.T.;
                                                                                                                                                                                                                         MEDLINE=88083942; PubMed=3691949;
                                                                                                                                                                                                                                         TISSUE=Lung;
                                                                                                                                                                                                                                                       SEQUENCE OF 676-1595 FROM N.A.
                                                                                                                                                                                                                                                                                 "Complete cDNA sequence of human alpha II fetal brain spectrin.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             TISSUE=Fetal brain;
Cianci C.D., Morrow J.S.;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                 "Generation of diversity in nonerythroid spectrins. Multiple polypeptides are predicted by sequence analysis of CNNs entempassing
                                                                                                                                                                                                                                                                                                                                                                                                                                   Moon R
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE 90170948; PubMed=2307671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa, Chordata; Craniata, Vertebrata, Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                               alpha-fodrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                            "Structure and evolution of a non-erythroid spectrin, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 IQTGSFDNNKAVLERRYSDFAKLQ---KALLKTFREEIEDVEFPRKHLTGNFAEEMICER
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                                                                                                                                                                                                                                                                                                                                                                          B: 01
                                                                                                                                                                                                                                                                                                                                                                        coding region of human nonerythroid alpha-spectrin."; Sicl Chem 266 4407-4433(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLGLQAFLQNLVAHKDIANCLAVREFL 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                   T., McMahon A
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                                                                                                                                                                Trans. 15:804-807(1987)
Giebelhaus D.H., Champion J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39153 MW,
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U
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; Pred. No. 0.4;
29; Mismatches
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BBE772299BA46FF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-erythroid alpha chain)
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(3)
   Bailes J.A.,
                                                                         of
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Lacey S.,

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Murakami N., Speed W.C., Seaman M.I., Zychowski P.L., Wetterbeig L., Pakstis A.J., Kidd JR., Kidd K.K.;

"Association and linkage analyses of the nonerythroid alpha-spectrin (SPTANI) gene on chromosome 9q34 with a large Swedish kindred.";

submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS THIS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Site-directed mutagenesis of alpha II spectrin at codon 1175 modulates its mu-calpain susceptibility.";
Biochemistry 36:57-65(1997).
                REPEAT
REPEAT
REPEAT
                                                                                                                                                                                     SMART; SM00054; EFh; 2.
SMART; SM000754; SH1; 1.
SMART; SM000150; SPEC; 20.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS0002; SH3; 1.
                                                                        REPEAT
REPEAT
                                                                                                                                                Cytoskeleton; Membrane, Calmodulin binding, Actin binding, Capping protein, Calcium-binding, Repeat, SH3 domain, PolyREPEAT 10 42 SPECTRIN 1.
                                                                                                                                                                                                                                                                                       Ptam; PF00018; SH3; 1.
Ptam; PF00036; efhand; 4.
Ptam; PF0045; spectrin; 32.
PRINTS; PR00452; SH3D0MA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J05243; AAA51790.1; -. EMBL; U83867; AAB41498.1; -. EMBL; M24773; AAA524681; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Rioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                ProDom; PD000012; EF-hand; 1. ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 182810
                                                                                                                                                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal brain;
MEDLINE=97146462; FubMed-8993318;
   DOMA I N
                                                             REPEAT
                                                                                                        REPEAT
                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1073-1349 FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 811-1529 FROM N A , VARTANT ILE-1300, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carritt B., Henchman S K , Moon R.T.;
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: RELONGS TO THE SPECTRIN FAMILY.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
SIMILARITY: CONTAINS 1 PANAIN
SIMILARITY: CONTAINS 23 SPECTRIN PEPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOSKELETON AT THE MEMBRANE.
SUBUNIT: LIKE ERYTHPOCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETRAMERS
                                                                                                                                                                                                                                                                                                                                                                                                      P07751; 1AEY.
4; HGNC+11273; SPTAN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       M18627; AAA51702.1, U26396; AAB60364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AF148808;
                                                                                                                                                                                                                                                                                                                                                   IPR001452; SH3.
IPR002017; Spectrin
                                                                                                                                                                                                                                                                                                                                                                                IPR002048; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF26672.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.241-241 (1987)
 676
782
888
955
1026
                                                                        465
571
                                                                                                                                              spectrin 1.
SPECTRIN 2.
SPECTRIN 3
SPECTRIN 5.
SPECTRIN 6.
SPECTRIN 7.
SPECTRIN 8.
SPECTRIN 8.
SPECTRIN 9.
SPECTRIN 10.
SPECTRIN 10.
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RESULT 11
SNXN_HUMAN
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Best Local &
Matches 69
                                                                 SAXN HUMAN STANDARD; FRT; 2
Q95L93; Q9H5U0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
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REPEAT
                  Homo sapiens (Human).
Eukarycta, Metazoa, Cherdata, Craniata, Vertebiata, Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                         Sorting nexin
                                                                                                                                                                 2112 EDLTD 2116
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NCBI_TaxID=9606;
[1]
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                                                                                                                                                                                                                                                                                         1935
                                                                                                                                                                                                                                                                                                                                 1878 N---VEEEEAWINEKMTLVASEDYGDTLAAIQGLLKKHEAFETAFTVIKDEVNEVCTNGQ 1934
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                                                                                                                                                                                                                                                                                                             139
                                                                                                                                                                                    289
                                                                                                                                                                                                                                                                                                                                                                                           37 PGPDGHLDTHSGLSSNSSMTTPELQQYWQNQKCFWKHVKII,FEIASAPIEEP-KVSKEVV 95
                                                                                                                                                                                                                                                                                                                                                                        PAIQGVLDTGKKLSDDNTIGKEEIQQRLAQFVEHWKELKQLAAARGQRLEESLEYQQFVA 1877
                                                                                                                                                                                                                                                                    ----GCTRAGQYERALELTLEVUPLOEKUTAHCPA-----AAVPALCAVLLUC-----
                                                                                                                                                                                                                                                                                                            EFPRKHLTGNFAEEMICEPPPALQEYLGLLYAIPCVPPSP----EFLDFLTRPELREAF 193
                                                                                                                                                                                                                                              IGEKENSLKTDDYGRDLSSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLLAAKHVQS
                                                                                                                                                                                                                                                                                                                                                     YQIIVIQTGSFDNNKAVL--ERRYSDFAKLQKALLK------TFREEIEDV----- 138
                                                                                                                                                                                                                                                                                                                                                                                                                 69;
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                                                                                                                                                                                                                            -HPDLDPPAEAFAAGERALQP--LQAPEGHRYYAPLLDAMVRLAYALGKDFVTLQ
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A -> D (IN REF. 2).
DG > EF (IN REF. 2).
V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N -> K (IN PEF 2)
F -> S (IN REF 2).
V -> I (IN REF 2).
Q -> QLSYLL (IN FEF 2).
F -> R (IN REF 3 AND 4)
N -> E (IN REF 2).
IA -> ED (IN REF 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECTRIN 18.
SPECTRIN 29.
SPECTRIN 21.
SPECTRIN 21.
SPECTRIN 22.
SPECTRIN 22.
SPECTRIN 23.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
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SPECTRIN
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SPECTRIN
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SPECTRIN
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T -> I.
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                           Craniata, Vertebrata, Euteleustumi;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 141;
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                                                                              update)
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www isb-sib ch/announce/or send an email to license@isb-sib.ch)
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Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hong W.; "A new member (SNX23) of the sorting nexin family."; "A new member (SNX23) to the EMBL/GenBank/DDBJ databases
               Sauerwald A , Hoesche C., Oschwald R., Kilimann M.W.; "The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-less, phylogenetically conserved sequence with cell
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                       Synapsin I (Brain protein 4.1).
CAAT-less, phylogenetically conserved sequence with cell type-specific promoter function.";
                                                            SEQUENCE OF 1-125 FROM N.A. MEDLINE=90368667; PubMed=2118519;
                                                                                                                                             MEDLINE=90243651; PubMed=2110562;
Suedhof T.C.;
                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; Protein transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., M
Nakajima Y., Mizumo T., Morinaga M., Tujiwar
Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T
Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE=Lung;
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 PRYSPEPEMHKT-LKLKYAELAALEEPPKKLEGNKDEPVIAEPPSHLEKYLRDEESV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 RRYSDFAKLQKALLKTFREEIEDVEFPRKHLTGNFAEEMICERRRALQEYLGLLYAI 171
                                                                                                             Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trafficking
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: May be involved in several stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                             structure of the human synapsin iol Chem. 265.7849-7852(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00787; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK026698; BAB15530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 42 1
24; Conservative
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BELONGS TO THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PX; 1
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P -> A (IN REF. 2)
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63
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A., Fujiwara T., Ono T.,
ri Y., Ota T., Suzuki Y.,
., Nakamura Y.,
                                                                                                                           protein.";
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EMBL; M58374; AAC41931
EMBL; M58375; AAC41931
EMBL; M58376; AAC41931
EMBL; M58377; AAC41931
EMBL; M58371; AAC40608
EMBL; AL009172; CAA156
PIR; A35363; A35363.
PIR; B35363; B35363.
DOMAIN
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

:- FUNCTION: NEURONAL PHOSPHOPPOTEIN THAT COATS SYNAPTIC VESICLES BINDS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE REGULATION OF NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
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modified and this statement is not removed. Usage by ar
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                                         NIWWOC
                                                                                        DOMAIN
                                                                                                                                                     Pfam; PF02078; Synapsin; 1. Pfam; PF02750; Synapsin C; 1. PRINTS; PR01368, SYNAPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                 DOMAIN
                                                                               DOMAIN
                                                                                                                  Synapse;
                                                                                                                              PROSITE;
                                                                                                                                                                                                                    Genew; HGNC:11494; SYN1.
                                                                                                                                                                                                                                 HSSP; P17599;
                                                                                                                                           PROSITE;
                                                                                                       lternative
                                                                                                                                                                                          interPro; IPR001359; Synapsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 265:14932-14937(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: SYNAPSE.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYNAPSIN IA (SHOWN HERE) AND SYNAPSIN IB, ARE PRODUCTS: 2 ISOFORMS; SYNAPSIN IB, ARE PRODUCTS: 1T IS PROBLED BY ALTERNATIVE SPLICING PIM: SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN KINASES. IT IS PROBABLE THAT PROSPORTLATION PLAYS A POLE IN THE REGULATION OF SYNAPSIN I IN THE NERVE TERMINAL.
SYNAPSIN I IN THE NERVE TERMINAL.
SYNAPSIN I IN THE NERVE TERMINAL.
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                                                                           Phosphorylation, tive splicing.
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                                                                                                               Repeat; Actin-binding
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                                                                AND SYNAPTIC-VESICLE
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VARSPLIC
                                                                                                                                                                                              Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMRL/GenPank/DDBJ databases.
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                trafficking (By similarity).
-!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY
-!- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                  Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21378165; PubMed=11485546;
Teasdale R.D., Loci D., Houghton F., Karlsson L., Glooson F.A.
"A large family of endosome-localized proteins related to sort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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16-00T-2001 (Rel
15-JUN-2002 (Rel
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16-00T-2001 (Pe
16-00T-2001 (Pe
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                                                                                                                                                   TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 358:7-16(2001).
                                  -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 PPPPGAHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSLSNAVKQTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGIPSVNSLHSVYNFCDKP-WVFAQMVRLHKKLGTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAVPALCAVLLCHRDLDRPAEAFAAGERALQRLQAREGHRYYAPLLD 271
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40, Last sequence update)
41, Last annotation update)
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24.0%; Pred. No. 1.
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MISSING (IN SYNAPSIN IB)
G -> E (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Indels
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                              215142, 216640, Q15148;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                             McLean W H I , Pulkkinen L., Smith F J.D , Pugg E L , Lane E B ,
Bullrich F., Burgeson R.E., Amano S., Hudson D.L., Owaribe K.,
McGrath J A , McMillan J B , Eady F.A J., Leigh I M , Christiano A M.,
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                   Vitto J.
                                                                                     MEDLINE=96312447; PubMed=8698233;
                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE
                                                                                                                                                          chromosome localization
                                                                                                                                                                                              Liu C
                                                                                                                                                                                                             MEDLINE:96210632; PubMed=8633055;
                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata,
Mammalia, Eutheria; Primates,
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                    Plectin 1 (PLTN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:14975; SNX11.
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                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                        Human piectin, organization of the gene, sequence
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                                                                                                                                                                                                                                                                                  TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPALELLLE
of plectin causes epidermolysis bullosa with muscular dystrophy
                                                                                                                                                                                         .-G., Maercker C., Castanon M .T., Hauptmann P.,
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                                                                                                                                                                                                                                                                                                                 Metazoa, Chordata, Craniata,
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Pulkkinen L , Smith F J.D., Shimizu H , Murata S , Yaqita H , Hachisuka H , Nishikawa T , McLean W.H.I., Uitto J , "Homozygous deletion mutations in the plectin gene (PLEC1) in patients with epidermolysis bullosa simplex associated with late-onset muscular dystrophy.";
Hum Mol Conce
                                                                                                                                                                                                                                                                                                                                             MUSCLE, HEART, PLACENTA AND SPINAL CORD.

DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH AUD THE COMMINI, GFAP, CYTOKERATINS, LAMIN B.

VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B.

PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS OR EB-MD). AN AUTOSOMAL RECESSIVE DISSOCIATE LATE-ONSET MUSCULAR DYSTROPHY.

INTERMEDIATE SIMILARITY: CONTAINS 1 ACTIN BINDING DOMAIN.

SIMILARITY: CONTAINS 2 CALPONIN HOMOLOGY (CH) DOMAINS.

SIMILARITY: CONTAINS 3 PLECTIN PEPEATS

SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deficiency.
Am. J. Path
                                                                                                                                         EMBL; X97053; CAA65765.1;
HSSP; Q01082; 1BKR.
Genew; HGNC 9069; PLEC1.
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Bauer J.W., Rouan
Muss W., Hametner
     Pfam; PF00307; CH; 2.
Pfam; PF00061; Plectin; 19.
Pfam; PF03501; S10_Plectin; 1.
SMART; SM00033; CH; 2.
                                                InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001101; Plectin_repeat.
InterPro; IPR005326; S10_plectin.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                            use by non-profit modified and this stentities requires a
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J. PATHOL 158:617-625 (2001).

J. PATHOL 158:617-625 (2001).

J. PATHOL 158:617-625 (2001).

J. PATHOL 158:617-625 (2001).

MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OF MICROFILMS SUCH AS ACTIN TO MEMBRANE COMPLEXES IN MISCLE MAY BE INVOLUED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE PROJUCTION OF THEIR DYNAMICS.

SUBUNIT: HOMODIMER OF HOMOTETRAMER,

ALTERNATIVE PRODUCTS: 3 ISOPOMES; 1 (SHOWN HERE), 2 AND 3; APE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN MICROFILM AND CORNAL PROPERTY.
                                                                                                                                                                                                                                                                                                   European
                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation services and bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way.
                                                                                                                                                                                   Z54367;
U53204;
U63610;
U63609;
                                                                                                                      226670
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J.W., Pouan F., Kofler B., Pezniczek G.A., Kornacker I.,
., Hamether R., Klausegger A., Huber A., Pohla-Gubo G.,
G., Uitto J., Hintner H.;
                                                                                                                                                                                                                                                           and this statement is not removed. Usage by requires a license agreement (See http://www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genet. 5:1539-1546(1996).
                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
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SMART; SM00150; SPEC; 5.
SMOSITE; PS00010; ACTININ 1;
PROSITE; PS00020; ACTININ 2;
PROSITE; PS00021; CH; 2.
PROSITE; PS00021; CH; 2.
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MISSING (IN MD-EBS).
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RPSPEPAPAT -> MSGEDAEVFAVSEUVSNUSSGSESPGD
TLPWNLGKTORSRRSGGAGSNGSVLDPAERAVIRIA (IN
ISOFORM 2 AND ISOFORM 3).
MISSING (IN ISOFORM 3).
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RQYLHLPPEIVAASL@EVERPVAMVMPARETPHV@AV@GPL
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16-00T-2001 [Rel. 40, Treated]

16-00T-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
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Mamma'lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  Homo sapiens (Human)
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                Craniata; Vertebrata; Euteleostomi;
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InterPro; IPR001683; PX.
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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARI

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# ALIGNMENTS

무	γ	Db	8	Db	δ	Ма	rg C	SQ	אַ אָנ	DR.	25	7 ;	R F	Ę,	RP :	RZ	26	3 6	80	DE	TQ	TU	Ü	AC	J.,	RESULT
124 IGDKSCHPKLAPFLEAHVPLSWPIGLDKPQSEAPLQALQEAGLTPTPPPPSLKELL 178	257 LQAREGHRYYAPULDAMVRIAYAIGKTEVTLGERIEESQLEKETERGITLKELT 310	64 TGLYREALALWANAWQLQAQLGTESGPDRPLLTLAGLAVCHQELEDEGEARACCEKALQL 123	198 AGQYERALELLIRVLELQEKI-TAHCEAAAVPALCAVLUCHRULDREAEAFAAGERALGE 256	4 ISFPRKRLARNETARTIARPSRAFEQFLGHLQAVPELRHAPDLQDFFVLPELRPAQSLTC 63	LLYAIR	10	Match 16.0%, Score	SEQUENCE 184 AA; 20612 MW; C3697FE2A1B19559 CRC64;	Pfam; PF00515; TPR; 1.	58570; AAG23773.1;	Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	man come crones		Qin W.X., Zhou X.M., Zhang F F., Jiang H Q., Huang Y , Wan D.F.,	SEQUENCE FROM N.A.		NCBI TaxID=9606;	Chordata, Craniata, Vertebrata, E			(TrEMBLrel. 21, Last annotation	20, Last	2002 (TrEMBLrel.		CAWY78 PRELIMINARY. PRT. 184 AA	Y78

311 VREYL

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                                                           Q9VQG1;
Q9VQG1;
01-MAY-2000
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CG3077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoud; Liauseus, Lings
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera, Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
CG 30 / 7
          CG3077 protein.
                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY061149; AAL28697.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0031457; CG3077.
InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 IKEVL 183
                                                                                                                                                                             277 TCAHLWWQRGQDQKPITDRLTD 298
                                                                                                                                                                                                            272 AMVRIAYALGKDFVTLQERLEE 293
                                                                                                                                                                                                                                                                                                          179 EYFLRFLQHDELTRACQFLDERRNEMAIPILENCFPLLNKIYMNPSPPVLLILCRLVAAC
                                                                                                                                                                                                                                                                                                                                           178 REFIDELTREELREAFGCLRAGQYPRALELLLRVLPLQEK-----
                                                                                                                                                                                                                                                                                                                                                                                                          118 SDFAKIQKALLKTFFREEIEDVEFPRYHLTGNEAEEMICERPPALQEYLGILYAIFCVPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                          59 AEYKPTTDGSTVLRFDILLAHIMPPDGEDVKIKPFVVYELTVKQDGATEDTQPAKIEPRY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 PITOCTARTQQEAPATGPDLPHPGPDGHLDT----HSGLSSNSSMTTRELQQ-YWQN-QK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PIHAVMAKPI.HHOPTFDGD--PPGPD-ELDSPAIEAAALDIPPPESDKALOKGVWERATS 58
                                                                                                                                                                                                                                            TSSPVPHHAAERWALLALSRFETLCDIDL----
                                                                                                                                                                                                                                                                                                                                                                            TOFRELYLGIKEOHPAEMANKYFPAKVLMGNFKSELIGERSAAFEAFLTYVASOAMLEDS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00787; PX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 20,
                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                           ----ALCAV----LLCHRDLDRPAEAFAAGERALQRLQAPEGHPYYAPILD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37252 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 210; 27.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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Last annotation update)
                          Last annotation update)
                                           Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6BA23C08D7F1:A62 CFC64;
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                                                                                          295 AA
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                                                                                                                                                                                                                                            ---LPLYIPLLH 276
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RX Adams M.D., Celniker S.E., Holf P. M., Hoskins R.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf P. M., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA Hardin J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C. Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxerdale J., Bayraktaroglu L., Bassley E.M.,
RA Harris W.J., Bernos P.V., Bernam B.P., Bhahdari D., Botcher A., Chardy
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Harris W.J., Bennes P. Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evaley S., Dahlke C., Davenport L.B., Davies P.,
RA Dephlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A. Howland T.J., Hernands J.A., Fee-hum K.A.,
RA Hostin D., Houston K.A. Howland T.J., Hernands J.A., Fee-hum K.A.,
RA Hostin D., Houston K.A., Howland T.J., Hernands J.A., Fee-hum K.A.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshina N.V., Mobarry C., Worlfor K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue H.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shur R.C., Siden-Kiamos D.A., Wenter R., Wang A.H., Wang X.,
RA Silbs R.A., Myers E. W., Phin C.M., Milssehach J., A.,
RA Yelly R. Weh R. F., Caveri J.S., Zhun M., Slasshach J., A.,
RA Silbs R.A., Saysaraman D.A., Wenter S., Mang J.N., Saith H.O.,
RA Silbs R.A., S
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00787; PX;
SMART, SM00312; PX;
SEOUENCE 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003582; AAF51213.1; FlyBase; FBgn0031457; CG307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota, Neoptera; Endopterygota, Diptera, Brachycera, Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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185 LNKIYMNPSPPVLLILC----PLVAACTSSPVPHHAAERWALLALSRFETLCDIDL
                                             195
                                                                                         135
                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [nterPro; IFR001683; PX.
                                                                                                                                                                           75
                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                               16
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                                                                                                                                                                                                                                                                                                         PGPDGHLDT----HSGLSSNSSMTTRELQQ-YWQN-QKCRWK----HVKLLFEIASARI
                                           LPAGQYPRALKILLRVLPLQEKLTAHCPAAAVP-----ALCAV----LLCHRDLDRPA 244
                                                                                  FPAKVLMSNFKSELIGEPSAAFEASL-----TACQELDERRNEMAIPILENCERL 184
                                                                                                                             FPRKHLTGNFABEMICERRRALQEYIGILYAIPCVRRSRBFI.D----FI.TRPELREAFGC
                                                                                                                                                                         MPPDGEDVKIKPEVVYELTVKODGATEDTOPAKIERRYTDERELYLGLKROHPAEMANKY 134
                                                                                                                                                                                                                  ----EERKVSKFVVYQIIVIQTGSF-DNNKAVLERRYSDFAKLQKALLKTFREEIEDVE
                                                                                                                                                                                                                                                             PGPD-ELDSPAIEAAALDIPPPESDKALQKGVWERATSAEYKPTTDGSTVLRFDILLAHI
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                      33532 MW; 7D7805C001B0F31D CRC64;
                                                                                                                                                                                                                                                                                                                                                                    11.2%;
27 7%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG3077.
                                                                                                                                                                                                                                                                                                                                                  3 B ;
                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                           Score 185.5;
                                                                                                                                                                                                                                                                                                                                                  Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                           Length 295;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                             74
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RESULT
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EMBL; AF001435; AAB81205.1; -.
InterPro, IPR001683; PX.
Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
Hypothetical protein.
SEQUENCE 152 AA; 17784 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            014612;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019833; AAM19823.1;
InterPro; IPR001683; PX:
Pfam; PF00787; PX;

Transparent Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit Profit 
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 17.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97397562; PubMed=9253601;
Guru S C , Agarwal S.K , Manickam P., Olufemi S.-E., Crabtree J.S.,
Weisemann J.M., Kester M., Kim Y.S., Emmert-Buck M.R., Liotta L.A.,
Spiegel A.M., Boquski M., Roe B.A., Collins F S , Burns A L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to chromosome 20 open reading frame 161.
                                                                                                                                                                                                                                                                                                                                                    "A transcript map for the 2.8-Mb region containing the multiple endocrine neoplasia type 1 locus.";
Genome Pes 7.72<-735(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.J., Chandrasekharappa S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPDQLPLGDGTSGEDAERSPPPDGQW------GSQLLARQLQDFWKKSRNTLAPQRLL 132
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      2B3AF6C5A77CB8EF CFC64;
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                         01-NOV-1999 (TrEMBLrel 12, Created)
01-NOV-1999 (TrEMBLrel 12, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
                      Arabidopsis thaliana (Mouse-ear cress) 
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; 
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 37.7 kDa protein.
                                                                                                                           AT2G15900
                                                                                                                                                  At2g15900 protein
                                                                                                                                                                                                                                                                                                              ©9XIM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00787; PX; 1.
Hypothetical protein.
SEQUENCE 337 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC016091; AAH16091.1; -. MGD; MGI:1916274; 1500032B08Rik InterPro; IPR001683; FX.
                                                                                                                                                                                                                                                                              Q9XIM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R., Strausberg (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91WE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=EYE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 --- RGGEVTRPSEVSRDLRILP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 GCLRAGOYPRALELL--LRVLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 -- RGGEVTRPLEVSRDLHILP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEFPAFPRAQVFGRFEASVIEERPKGAFDLLRFTVPIPALNNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VE----FPRKHLTGNFAEEMICERPRALQEYIGILYAIPCVPRSPEFINFLTRPELREAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVSDPRTHPKGYTEYKVTAQFISKKDPEDIKEVVVWKRYSDFRKLHGDLAYTHRNLFRR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 7.4%, Score 122, DB 4, Length 152;
Similarity 27.5%; Fred. No. 0.0075;
39; Conservative 24; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND RETINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
Brassicales, Brassicaceae, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37742 MW; 743923E18ED9EF4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100, DB 11, Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                           FET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                           952 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Indels
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                                Rosidae;
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE-20083487; PubMed:10617197;
Lin X., Kaul S., Pounsley S. D., Shea T. P., Benito M.-I., Town G. D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C. P., Ketchum K. A., Lee J. J., Ponning G. M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S. E., Ilmayam L., Tallon L.J., Gill J.E.,
Adams M. D., Carrera A. J., Creasy T. H., Goodman H. M., Somerville C. P.,
Adams M. D., Carrera A. J., Creasy T. H., Goodman H. M., Somerville C. P.,
Copenhaver G. P., Preuss D., Nierman W. C., White O., Eisen J.A.,
Salzberg S. L., Fraser C.M., Venter J.C.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                 InterPro;
InterPro;
                                                                              EMBL;
                                                                                                                          STRAIN=972;
McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
    Pfam; PF00787;
Pfam; PF02194;
                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                             Hypothetical 117.0 kDa protein C16All 04 in chromosome SPCC16All.04.
                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN 2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                            Q9USN1;
01 MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02194; PXA; 1.
SMART; SM00312; PX; 1.
SMART; SM00313; PXA; 1
                                                                                                        Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI TaxID=4896;
                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                           Q9USN1
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InterPro; IPP001683, FX.
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                                                              InterPro; IPRO01683; PX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin X.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 DV---ENKTWEVKRRYSNEERLHRQL-----KEÏPNYNLQLPPKRIFSSSTEDAFVHPRC 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 HNDNY1SDNKSQSIVIHKEGOHCLKLKČR-----VLGAYFEKQGSKSFAVÝSÍAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 IQLDKYLQDLLCIANVAEQHEVWDFLSAASKNYSFG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 RALQEYLGLLYAIRCVRRSREFLDFLTPPELPEAFG 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                           SIMILARITY: TO YEAST MDM1
%L; AL109957; CAR53076 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTGGFDNNKAVLERFYSDFAKLQKALLKTFPERIE--DVEFPRKHLTGNFAEEMIGERR- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
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IPR000142; Regl Sprotein.
0787; PX; 1.
2194; PXA; 1.
                                                IPR003114; PX_assoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             952 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TORTH MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1%; Score 117; DR 26.3%; Pred. No. 0.2;
                                                                                             MDM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                               Schizosaccharomycetes;
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                                                                                                                                        Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                           1010 AA.
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                                                                                                             databases
                                                                                                                                          Zimmermann
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RESULT 9
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Best Local
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01-DEC-2001 (
01-DEC-2001 (
01-JUN-2002 (
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CARBOHYD
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CARBOHYD
CARBOHYD
CAPBOHYD
                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K Yu C., Lewis S. E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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DOMAIN
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SMART; SM00312; PX; 1.
SMART; SM00313; PXA; 1.
SMART; SM00315; PGS; 1
ATP-binding; Tr
                                    Prodom; PD000001; Euk_pkinase; 1.
FROSTE, FS50011, PROTEIN_KINASE_DOM; 1.
                                                                                    Ffam, PF00069, pkinase; 1. Ffam, PF00787; PX; 1
                                                                                                                                               FlyBase; FBgn0033244, CG8726.
InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                     STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eterygota; Neoptera, Endopterygota, Dip
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera, Endopterygota, Diptera, Brachycera, Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG8726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LD23236p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95RK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein, TRANSMEM 6 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE,
                                                                                                                                 InterPro; IPR000719; Euk
InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AIRCVERSREFLDFLTRFELR EAFGCLRAG OYFRALELL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      736 WMV-ARRYREFAELHKQLKQTY-PGVPSLKFFQKSIITSLNKNVLEYPRGALEEYLQSLF 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 RMPEVODSEMLEMELSOCHITAROMEMBEEVGEEWEQLLEVE 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA PELZOYMONOKOPMKHYKLEFETASARTEEPKVSK-----PVVYQTTV TETESEDNN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POPDOYMSOEE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAVLERRYSDFAKLOKALLKTEREEIEDVEEPRKHLTGNEAEEMICERPRALQEYLGLLY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50132, RGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1010 AA,
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    Transferase.
50 AA; 50748 MW;
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27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSKLENPSRVSIDSEKISKEENTPDFAVYTIPIEPLENGHVPSG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116992 MW; ZABD19194177F1DB CRC64,
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 3; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
DIBABF8CEFE27E15 CRC64;
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                                                                                                                                                                                                                                                          Phouanenavong S., Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachycera, Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1010;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable flaggllar assembly protein FLIH.
FLIH OR RSP0392 OR RS00820.
Palstonia sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8XSS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid megaplasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 RRALOEYLGLLYAIRCVRRS---REFLDFLTRPE-----LREAFGCLR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the plant pathogen Ralstonia solanacearum.";
NATURE 415:497-502(2002).
EMBL; AL646078; CAD17543.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-GMI1000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 KQALQEYINAVLMNPILASSLPAKREVD----PESYSQSFHDHAVQNAMLCLR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 LLRVWRGASNKNYWTVLRRYNDFDRLDKSL----RVSGTELPLPRKRIFGNMRPBFTAER 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 IIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREETEDVEFPRKHLTGNFAEEMICER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000563; Flag_FliH.
                                                                                                                                                                                                 126 ALLKTERBEIEDVEFPRKHLTGNFAEEMICERRRALQEYLGLLYAIRCVRRSREFLDFLT 185
                                                                                                                                                                 134 -----GALRÀ--QPE-----RILPLVREVLGDAPTÄPAPÄMLRVHADDAELIRQÄL 177
                                                                                                                                 186 RPELREAFGCLRAGQYPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDLDRPA- 244
                                                                                                                                                                                                                                                                                                16 HEWER ... IDEVPOARLAAAAAAP--PPPPPBBBBBBBBBBS-----BEEWO 57
     293 ESQL 296
                                                                                                                                                                                                                                                                66 NQKCRWKHVKLLFEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQK 125
                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                  58 -----AMLEAELANARDEGRRDGFAQGFQ-----DGFEQGR----PQGEEDSRQIA 99
                                                                                                                                                                                                                                                                                                                                 6 HPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTRELQQYWQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Conservative
                                   GTELAAAGWTLVVDAAIERGGCRVQTRFGET-DATLQTRWAELTRALGRDTAWIASERVE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF02108; FliH; 7
                                                                  --EAFAAG-----ERALQRLQAREGHRYYAPLLDAMVRLAYALGKDFVTL-QERLE 292
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome 248 AA; 26993 N
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       26993 MW;
                                                                                                                                                                                                                                                                                                                                                                                        24.0%;
                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 115; DB 1
24.0%; Pred. No. 0.056;
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                                                                                                                                                                                                                                                                                                                                                                          40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         9CA196E0BC549D47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 248;
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                                                                                                                                                                                                                                                                                                                                                                            99; Indels 92; Gaps
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Richards S.A., Ashbunner M., Hendersen S.W. RA George R.A., Lewis S.E., Richards S.A., Ashbunner M., Hendersen S.W. RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Pfeiffer B.D., Ra Baradon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Welson C.P., Maldwin D. Ra Ballew R.M., Basu A., Baxera E.G., Helt G., Welson C.P., Maldwin D. Ra Ballew R.M., Basu A., Baxeradale J., Bayraktaroglu L., Beasley E.M., Ra Ballew R.M., Basu A., Butler H., Cadlau E., Center A., Chandra I. Burtis K.C., Busam D.A., Butler H., Cadlau E., Center A., Dietz S.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S., Ra Beeson K.Y., Benos P. Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borthin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borthin K.J., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J. M., Kalush F., Karpen G.H., Ke Z., Kennison J. M., Kalush F., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Harko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Harlov G., Milshina N.V., Mobarry C., Morris J., Mosprefi A., Ra Merinlov G., Milshina N.V., Mobarry C., Morris J., Mosprefi A., Ra Manja C., Stocheler F., Shen H., Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., Shith T., Ra Ayli Lasko P., Lei Y., Massarman D.A., Weinstock G.M., Waissenbach J., Ra Ayli Y., Waissarman D.A., Weinstock G.M., Waissenbach J., Ra Ayli K., Sandre F., Zahon M., Zhang G., Zhao Q., Zheng L., Wang S., Hang S., Yao Q.A., Yang S., Hang S., Pao Q.A., Weinstock G.M., Waissenbach J., Ra Kohner M., Scheler F.
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01-MAY-2000
01-JUN-2002
                                           Matches
                                                                            Query Match
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Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
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                                                                                                                                          InterPro; IPR001683; PX.
InterPro; IPR000159; RA_domain.
Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                         FlyBase; FBgn0029794; CG3138.
                                                                                                                                                                                                                                               HSSP; Q12923;
                                                                                                                                                                                                                                                                EMBL; AE003435; AAF46070.1; -.
23 TOORAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQXCRWYHVKLLFEIAS 82
                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TaxID=7227;
                                           44;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                        431 AA; 49535 MW; 9E5F03709DA2F697 CRC64;
                                              Conservative
                                                               6.9%; Score 114.5; Di
25.9%; Pred No. 0.12;
                                                  20;
                                                  Mismatches
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                                                    63; Indels
                                                                                              Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Kawai I Shinagawa A, Shihata K, Yoshino M, Itoh M, Ishii Y, RA Arakawa T, Hara A, Fukunishi Y, Konno H, Adachi J, Fukuda S, PA Arakawa K, Izawa M, Nishi K, Kiyosawa H, Kondo S., Yamanaka I, Raiyawa K, Izawa M, Nishi K, Kiyosawa H, Kondo S., Yamanaka I, Raiyawa K, Izawa M, Nishi K, Kiyosawa H, Kondo S., Yamanaka I, Raiyawa K, Itohaka H, Gojobori T, Pono H, Kasukawa T, Sairo P, Raiya H, Kondota K, Matsuda H, Ashburner M, Batalov S, Gasavant T, Pelischmann W, Gaasterland T, Gissi C, King B, Kochiwa H, Ra Kuchi P, Lewis S, Matsuo Y, Nikaido I, Pesole G, Quackenbush J, Karimi I.M., Staubli F, Suzuki R, Tomira M, Wagner L, Washio T, Ra Sakai K, Okido T, Phinno M, Aono H, Baldarelli R, Barsh G, Ra Brownstein M, J, Bult C, Fletcher C, Fujta M, Gariboldi M, Rownstein M, J, Bult C, Fletcher C, Fujta M, Gariboldi M, Karimorich S, Hill D, Hofmann M, Hume D A, Kamiya M, Lee N H, Lyons P, Marchionni L, Mashima J, Mazzarelli J, Mombaerts P, Ra Gansaki H, Saro K, Schoenbach C, Seya T, Shibata Y, Storch K, Fr. Ra Sanaki H, Saro K, Schoenbach C, Seya T, Shibata Y, Storch K, Fr. Ra Kunshiaw Boris A, Yoshida K, Hasegawa Y, Kawaji H, Kohtsuki S, Parakari M, Maraki Y, Yoshida K, Hasegawa Y, Kawaji H, Kohtsuki S, Parakari M, Kohtsuki S, Karima K, Maraki Y, Kawaji H, Kohtsuki S, Parakari M, Maraki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki Y, Kantaki 
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last sequence update)
5730433116Rik protein (2810011K15Rik protein).
5730433116RIK OR 2810011K15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK012711, BAB28427.1, ...
MGD; MGI-1916476; 2810011K15Pik
MGD; MGI:1922957, 5710471716Fik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9CRB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK017610; BAB30938.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPPOOTAR; PX. Pfam; PFOOTAT; PX; 1
111 AESC 114
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                                                      192 AFGC 195
                                                                                                                                                        139 EFPRKHLTGNFAEEMICERPRALOEYLGLLYAIPCVPRSRE----FLDFLT----RPELRE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14) KHILTGNF----AEEMICEPPRALQEYLGLLYAIRCVRRSREFLDFLTRPE 188
                                                                                                    57 EIPSKHVR-NWVPKVLEQRRQGLETYLQAV----ILENEELPKLFLDFLNVRHLPSLPK 110
                                                                                                                                                                                                                                                                        80 IASARIEERKVSK-FVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIEDV 138
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGIVNRNGERYIVFNIHMA-----GPQLCSPRYREFANLHSLL----PKEFSGFNFPK 123
                                                                                                                                                                                                                 IPSERHEDSDIEPGYTVFKIEVIMNG----RKHFVEKRYSEFHALHKKLKKC----IKTP 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00312; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA,
                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 113;
31 5%; Pred No (
                                                                                                                                                                                                                                                                                                                                                                                                                                         19652 MW;
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                                                                                                                                                                                                                                                                                                                            23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         076416D452392D69 CRC64,
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                                                                                                                                                                                                                                                                                                                                                   051;
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RESULT 13
Q90990
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Q941X3
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Best Local :
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01-DEC-2001 (TrEMBLrel. 01, Last sequence update)
Nonerythroid alpha-spectrin mRNA (Fragment).
Gallus gallus (Chicken).
Eukaryota: Mores---
                                                                                         Q941X3, PRELIMINARY;
Q941X3, O1941X3,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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                                            Oryza sativa (Rice)
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Birkenmeier C_S., Podine D M., Pepasky E.A., Helfman D M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae
Ehrhartoideae; Oryzeae; Oryza.
                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                B1088C09.3
                                                                          B1088C09.3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00435; spectrin;
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HSSF; P07751; 1AJ3.
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Proc Natl Acad Sci U S.A 82.5671-5675(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hughes S.H., Barker J.E.; "Remarkable homology among the internal repeats of erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                             430 SWFENAEEDLTD 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR002017; Spectrin
                                                                                                                                                                                                                                                                           282 KDEVTLOERLEE 293
                                                                                                                                                                                                                                                                                                          370 AAKHIQSKAIEVRHASLMERWNQLLANSAAFEKELLEAQEHFFEVEELFLTFAEEAASAFE 429
                                                                                                                                                                                                                                                                                                                                                                       310 ADVVESWIGEKENSLKTUDYGRFUSSVØTLIJTKØRTFPAGLJAPJJEGIANITALKIQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        KKNNHHVENITAKMKGLKGKVSDLEKAAAQPKAKLDE------NSAFLQENWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
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473 AA;
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21.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Mismatches
                                                                                              Last annotation update)
                                                                                                            Last sequence update)
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Pred. Nc. 0.28;
44; Mismatches 134; Indels 6
                                                                                                                             Created)
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                                                                                                                                                             PRT;
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Q91WB6
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Best Local
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ20335.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki T., Matsumoto T., Yamamoto K.;

"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,

clone:B1088C09.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AP003734; BAB68097.1; ...
InterPro; IPR001064; Crystallin.
InterPro; IPR001863; PX.
InterPro; IPR00683; PX.
Pfam; PF00787; PX; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                               EMBL; BC016131; AAH16131.1; --
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001683; px.
InterPro; IPR003124; WH2.
                                                                                                                    ProDom; PD000001; Euk_pkinase; 1.

PPOSITE; PS5011; PS0TEIN FINASE DOM; 1.

ATP-binding; Hypothetical protein; Transferase
SEQUENCE 582 AA; 65201 MW, ED55496B61F2E9AA CRC64;
                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1. Pfam; PF00787; PX; 1. Pfam; PF02205; WH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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24.5%; Pred. No. 0.39;
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36.4%; Pred. No. 0.48;
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3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARI

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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a human PSGL-1 binding protein.
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WPI, 2001-616502/71
                                                                                                     Lorenz M,
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                                                                                                                                                                                                      (GEMY ) GENETICS INST INC.
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                                                                                                Kriz R, Weich N,
                                                                                                     Shaw GD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PSGL-1) binding protein. The protein is a member of the selectin liquand interactor cytoplasmic (SLIC-1) family. The SLIC-1 polynucleotides and polypeptides are useful as targets for developing modulating agents to regulate a variety of cellular processes such as signal transduction, cytoskeletal organization, immune and inflammatory responses, interand intra-cellular communication, adhesion, migration, cell activation,
                                                                                                             Human; inflammatory bowel disease 1 protein, IBD1, IBD1prox, intestinal inflammatory disease; apoptosis, NF kappa B, cancer; inflammatory disease; immune disease; cryptogenetic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth, differentiation and proliferation. The SLIC-1 proteins provide novel diagnostic targets and therapeutic agents to control or modulate SLIC-1 molecule-associated disorders such as an inflammatory or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein ligand (PSGL-1) binding protein, useful as targets for developing modulating agents to regulate a variety of cellular processes including signal transduction -
                                                                                                                                                                                                                                              03 JAN 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                system disorder, a cardiovascular disorder, a cellular proliferation, activation, adhesion, growth, differentiation or migration disorder or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI65832
               FR2806739-A1
                                                                                                                                                                                                Amino acid sequence of IBD1prox protein.
                                                                                                                                                                                                                                                                                        AAG79120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Fig 1; 108pp; English.
                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                             AAG79120 standard; Protein; 334 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotides (SLIC-1) which enrode novel P-selectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 100.0%; Score 1650; DB 22; Local Similarity 100.0%; Pred. No. 2.3e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTREL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDFLTRPELREAFGC1.FAGQYPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRPAEAFAAGERALQRIQAREGHRYYAPLLDAMVPLAYALGKDEVTLQERLEESQLRRPT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRPAEAFAAGERALORLOAPEGHRYYAPLLDAMVPLAYALGKDHVTLOEPLEESOLERET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKLOKALLKTEREEIEDVEFPRKHLTGNFABEMICERRPALQEYLGLLYAIRCVRRSREF 180
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                                                                                              rectocolitis;
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                                                                                              Crohn's disease; Blau syndrome
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RESULT 3 AAB43067 ID AAB4

AAB43067 standard; Protein; 148

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source of (anti)sense oligonucleotides, for recombinant production of polypeptides, and in screening for interactive compounds. The polypeptides are used to raise specific antibodies which useful for diagnostic detection or purification of IBD1 and IBD1prox, to screen for specific binding agents, potential therapeutic agents. The IBD1 and IBD1prox polynucleotides and polypeptides are useful for treatment and prevention of inflammatory and/or immune diseases or cancer, where associated with mutations in genes corresponding to IRD1 and IRD1prox, especially cryptogenetic inflammation of the intestines (hemorihagic rectocolitis, Crohn's disease and Blau syndrome).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease. The IBD1 gene is probably involved in regulation of apoptosis and activation of NF-kappa B. The IBD1 and IBD1prox polynucleotides are is useful as source of probes and primers, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human protein designated IBD1prox. The IBD1prox protein is in proximaty to a gene encoding inflammatory bowel disease 1 (IBD1) protein, which is associated with intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 73-74; 97pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human nucleic acids associated with intestinal inflammatory
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                                                                                                                                                                                                        DRPAEAFAAGERALQRLQAREGHRYYAPI.LDAMVRLAYALJGKDFVTLQERLEESQLERPT
                                                                            PRGITLKELTVREYLH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKLQKALLKTEPEETEDVEEPPKHLTGNFAEEMTCEPPPALQEYLGLLYATPCVPRSPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKLOKALLKTEPEETEDVEFPPKHLTGNFAEEMTCEPPPRALOFYLGLLYAIRCVPRSPEF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQYWQNQKCRWKHVKLLFEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDF 120
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PRGITLKELTVREYLH 334
                                                                                                                                                    DEPASAFAAGSEALQEUQARBGHEYYAPILIDAMVELAYALGKLEVTLQEELESQLERET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1650; DB 22; Fred. No. 2.5e 163;
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08-FEB-2001 (first entry)

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cc antipsoriatic; antiparkinsonian; notropic; immunosuppressant; corresponding; anticonvulsant; antiarthritic; immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; coagulant; vasotropic; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; communostimulant; hypotensive; dermatological; immunosuppressive; coantiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; coagulant; hypotensive; dermatological; immunosuppressive; coantithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OPFX-associated disorder. The nucleic acids can be used to express OPFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritts, graft vs host disease, cardiovascular disease, diabetes mellitus, typertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allocaterial or fungal infection, malaria, autoimmune disorders, asthma, collectrial or fungal infection, malaria, autoimmune disorders, asthma, concturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antianaemic; gene therapy; cancer; prollierative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus, hypothyroidism, SCID, AIDS, cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cyrostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127736.
05-APR-1999; 99US-0127728.
30-MAP-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 4838-4839; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulperary; antipsoriatic; antiparkinsonian, nootropic, neuroprotective; vulperary; antipsoriatic; antiarchritic; immunosuppressant; cardiant; osteopathic; antiarchritic; immunosuppressant; cardiant;
                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal, antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX ORF2831 polypeptide sequence SEQ ID NO:5662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; thrombolytic;
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              Conservative
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                                                    95.5%;
         1; Mismatches
                                               Score 464, DB 21,
Pred. No. 4 4e-40;
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                                                                                          Length 148;
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19-MAY-2000;
07-JUN-2000;
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17-MAR-2000;
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2000US-0225213
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2000US-0225266
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8-0228924.
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                                          expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) proteins and polynucleutides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleutides may be used to prevent, proteins and treat immune/haematopoietic-related discusses, especially cancers and cancer metastases of haematopoietic artised genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences firm the present invention. AAK54921 to AAK94950 and AAM82169
                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM93921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis at treatment of diseases associated with inappropriate (I) expression. For
Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Rucleic acids encoding human immune/humatupuletic untigen polypeptidec, useful for preventing, diagnosing and/or treating cancers and
                               represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                 example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 16601; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                      metastasis
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156 AA;
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Human cancer cell growth inhibitor related protein SEQ ID NO:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human proteins capable of acting as cancer cell growth inhibitors. These can be used to inhibit cancer. The present sequence a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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             30-MAR-2001; 2001WO-US08631
                                      11-0CT-2001
                                                            WO200175067-A2
                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forension food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                          Novel human diagnostic protein #27885.
                                                                                                                                                                                                              ABG27894 standard; Protein; 580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 14 (Disclosure); 31pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human protein, and the polynucleotide that encodes it, useful for inhibiting cancer cell growth \,\, -
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WO200157182-A2 Homo sapiens Human immune/haematopoietic antigen SEQ ID NO:11983.

cytostatic; gene therapy; vaccine; metastasis

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

07-NOV-2001

(first entry)

AAM84390;

AAM84390 standard; Protein;

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CC polypeptide (II) sequences. (I) is useful as hypridisation probes, CC polypeptide (II) sequences. (I) is useful as hypridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. 10 and 10 and 10 acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
350 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLD
                                             1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLD 44
                                                                                                                      Local Similarity
                                                                                                                                                                                               580 AA;
                                                                                               Conservative
                                                                                                                   15.5%,
                                                                                                                   Score 255, DB 22; 
; Pred. No. 2.1e-17;

    Mismatches

                                                                                                                                          Length
                                                                                               Indels
                                                                                             Gaps
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2000IIS-0184664
2000IIS-0184876
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2000IIS-0190076
2000IIS-01900467
2000IIS-020447
2000IIS-0214886
2000IIS-0216647
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-2000; -2000; -2000; -2000; -2000;

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20.0CT                Mucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                               WPI; 2001-483426/52
M FSDB, AAK57171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                    Disclosure; SEQ ID NO 5667; 21pp + Sequence Listing; English
                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                             N-PSDB; ABL03728
                                                                                                                                                                                                                                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB59625 standard; Protein; 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 11983; 3071pp + Sequence Listing; English.
   insecticides,
                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                           interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHL 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 AA;
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2000US-0614150
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therapeutics and pharmaceutical
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                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                    detection reagent for detecting 1000 for elucidating cell signalling and
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Pred No. 6.1e-18
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                                                 The invention
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #23116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG23125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct
                         Claim 20;
                                                   biodiversity
                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                     SEQ ID No 53484, 103pp; English
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27.7%;
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The invention relates to isolated polynucleotide (I) and

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and or disorders in products dependent on DNA and anino acid sequences. ABG00010-ABG3077 represent novel human diagnostic amino acid sequences.
              17 JAN 2001; 2001WO-11901112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCP) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags polymucleotides.
                                                                                                           WO200154733-A1
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                       reproductive system; gastrointestinal; liver disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel signal transduction pathway protein, Seq ID 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ttp.wipo.int/pub/published_pct_sequences
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28.2%; Pred. No 0 00016;
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Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immun
                                                        N-PSDB; AAS27404.
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                                                                                                                                         SCI INC
                                                                                                         Ruben SM
 including cancers, immune
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel isolated polypeptides (I), and C polynucleotides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune CC transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), biewding disorders, haemoglobin abnormalities and GC (e.g. hepatitis C), biewding disorders, haemoglobin abnormalities and CC disorders, primary haematopoietic disorders, hyperproliferative CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative CC disorders (e.g. Gaucher's disease), rarkinson's disease), chromosomal CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal CC disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. disorders), respiratory disorders, dermatological disorders (e.g. disorders), respiratory disorders, dermatological disorders (e.g. disorders), repoductive system disorders, gastrointestinal CC disorder (inflammatory disorders), liver disorders, gastrointestinal CC disorder (inflammatory disorders), liver disorders, activators of T-cells, to induce higher affinity antibodies, and as a means to induce curpoliferation in pathologies e.g. acquired immune deficiency compatives pathway protein, amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 1052; 880pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders and neuronal disorders
                   Venter JC,
                                                                                                                                                                                                                    W0200171042-A2
                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 5778
                                                      (PEKE ) PE CORP NY
                                                                                      23-MAR.2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                           23-MAR-2001, 2001WC-US09231
                                                                                                                                                                                   27-SEP-2001.
                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                      26-MAR 2002
                                                                                                                                                                                                                                                                                                                                                                                                                         ABB59662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB59662 standard; Protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AESC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 AFGC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 TASARTEERKVSK-FVVYOTTVTOTGSFDNNKAVLERRYSDFAKLOKALLKTEREETEDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIPSKHVR-NWVPKVLEGRRGSLETYLGAV----ILENEELPKLFLDFLNVRHLPSLPK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFPRKHLTGNFAEEMICERRRALQEYLGLLYAIRCVRRSRE----FLDFLT---RPELPE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPSERYEESDLEFGYTVEKIEVLMNG----PKHEVEKPYSEFHALHKKLKKG----IKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                   Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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32.3%; Pred. No. 0.00071;
ative 22, Mismatches 40
                 Li PWD,
                 Myers EW;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; immunosuppressive, antiarthritic, antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
WPI; 2000-611712/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB45187 standard; Protein; 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDH; ABL03765
                                                            Rosen CA,
                                                                                                                                                                                           26 MAR 1999;
17 DEC-1999;
                                                                                                                                                                                                                                                                                         22 - MAR - 200u;
                                                                                                                                                                                                                                                                                                                                                         05-OCT 2000
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200058467-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system disorder; aging; chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein sequence encoded by gene 15 SEQ ID NO:128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 5778; 21pp + Sequence Listing, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ttp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 KHLTGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 TOQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTKELUUYWUNQKCRWKHVKLLFEIAS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 YGIVNRNGERYIVENIHMA-----GRQLCSPRYPEFANLHSLL----RKEFSGENFPK 123
                                                                                                                                                                                        DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIEDVEFFR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQQEADRLEPQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LPGKWPFQLSEQQLDTPPRGLEQYLEKVCAVPVIAESDAVQDFLTDTE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                         2000W0-US07505
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                                                                                                                                                                                           99US-0172410.
                                                                                                                                                                                                                         99115-0126502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EDQSGYSYIDYSDKRSLP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63,
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cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-CROSAN and AAB45114 represent segmences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic, antiproliferative, cytostatic; cardiant; vasotropic; cerebroprotective, nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 28; 440pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC80545.
                                                                                                       the invention.
                                                                                                                                                           used in the isolation and characterisation of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptides can also be used to aid wound healing and epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the breast or liver, cardiovascular disorders e.g. cardiac arrest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonists and agonists may be useful in treating, preventing and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungicide; and opthalmalogical. The secreted proteins, polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's diseases and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          their activities include immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms
168 AA;
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В
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                  Query Match
135 ESD 137
                              186 RPE 188
                                                                                             130 TERRETEDVEROPKHUTG----NEAEEMICEPSPALCEYLGLLYAIRCVPPSPEELDELT 185
                                                                                                                                                               70 RWKHVKLLEEIASARIEEPKVSKEVVYQIIVIQTGSEDNNKAVLEPRYSDEAKLQKALLK 129
                                                                                                                                                                                                                  Local Similarity
                                                               79 ---KREFANFTFPR--LPGKWPFSLSEQQLDARPPGLEEYLEKVCSIPVIGESDIMQEFLS 134
                                                                                                                                 RYKHV------EPAILHONL-- 78
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                 28.5%;
                                                                                                                                                                                                                                  6.8%;
                                                                                                                                                                                                                  Score 112.5, DB Pred. No. 0.0025
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                 37,
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                Length 168,
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ABB08158
                                                                                             hepatetropic, antiinflammatory, antipsoriatic, cytostatic, vir anticonvulsant; cerebroprotective; nootropic; neuroprotective, antiparkinscrian, transjenic, gene therapy.
                                         WO200242330 · A2
                                                                                                                                         Cytoskeleton-associated protein; CSAP; antiarteriosclerotic; human;
                                                                                                                                                                      Human cytoskeleton-associated protein (CSAP)-2 (ID: 959690CD1)
                                                                                                                                                                                                                                                            ABB08158 standard; Protein; 541 AA
                                                                   Homo sapiens
                                                                                                                                                                                                  (first entry)
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30-MAY-2002

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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT:2000;
08-NOV-2000;
07:DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and modulators are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CSAP, where the disorders are selected from a cell proliferative disorders such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, cancer, a viral infection such as those caused by adenoviruses, herpesviruses, and retroviruses, and a neurological disorder such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, dementia, and Parkinson's disease. The polymentides are also useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. The present sequence represents a human CSAP-2 polymentide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ding L, :
                        Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; heumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Altheimer's disease; Parkinson's disease; neurodegenerative disorder; Altheimer's disease; renal disorder; chromosommal abnormality. Down synfrome; ischaemia; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human cytoskeleton-associated proteins (CSAP) and encoding polynuclectides. The CSAP polypeptides can be expressed by standard recombinant methodology. The CSAP polynucleotides, polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytoskeleton-associated protein, useful in diagnosis, prevention or treatment of cell proliferative disorders, viral infections and neurological disorders.
           cardiovascular;
                                                                                                                                                                                               Novel signal transduction pathway protein, Seg ID 1046.
                                                                                                                                                                                                                                               07-NOV-2001
                                                                                                                                                                                                                                                                                                                              AAU17481 standard; Protein; 141 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-00T-2001; 2001WO-US50983.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- KPREANETEPP--LPGKWPESLSEQQUDAPPPGLEEYLEKVCSIPVIGESDIMQEPLS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AHHAd
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                                                                                                                                                                                                                                                                                                                                                                                                                                          266
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ue H, Tang YT, Lal PG, Batra S, Lu D
Ramkumar J, Griffin JA, Gururajan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 AA;
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; 2000US-247370P.
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abn-rmality, Down syndrome, ischaemia; rena
lar: respiratory: wound healing, endocrine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No 0.014;
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Lu DAM, s
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Sanjanwala
         Addison's disease
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      07.JUL.2000

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2000US-0224519.
2000US-0225114.
2000US-0225514.
2000US-0225566.
2000US-0225566.
2000US-0225568.
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2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0227182.
2000US-0227009.
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2000US-0232080
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2000US-0231242
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2000US-0229287
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2000US-0184664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. wound healing, epithelial cell proliferation, endoctine disorders (e.g. addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (ALES). AAU/059-AAU/1683 represent novel signal transduction syndrome (ALES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood related disorders (sickle cell anaemia), mycloprolificative disorders, primary haematopoietic disorders, hyperprolificative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel isolated polypeptides (1), and polymuclectides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune
                    WO200175067-A2
                                                                                                                     Human, Chromosome mapping, gene mapping, gene therapy, forensic;
                                                                                                                                                                   Novel human diagnostic protein #22886.
                                                                                                                                                                                                                  18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplant rejections and graft versus host disease,
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                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                       ABG22895 standard; Protein; 166
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                                                                                                                                                                                                                                                                                                                                                                                                                 102 ONKY-POVRAYNÉPŘKATŠNKDAKEVEÉPŘKOLONÝL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LKTFREEIEDVEFPRKHLTGNFAEEMICERRRALQEYL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.68, Local Similarity 25.98, nes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GPITQCTAFTQQEA----PATGP-DUPHFGPDGHLDTHSGLSSNSSMTTPELQQYWQNQ 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GPGSQSSPRVPDEAGAHFSPGTVPGTJSQTSEDQSL-----SDFEISNPALINVW---
                                                                                                     supplement, medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -IPSVFLRGKAAXAFHVYQVYI----RIKDDEWNIYRRYTEFRSLHHKL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Scare 108.5, DB
, Pred. No. 0.0051;
21, Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide (II) sequences. (II) is useful as hybridistation probes, (from polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in vecembinant production of (II). The complex composition of the polymerase states are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (II): (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations compositions of the polypeptide and polynuclectide sequences have applications in CC and to produce other types of data and products dependent on DNA and composition acid sequences. ABG00010-ABG30377 represent novel human conditions acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO care fits wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.5%; Score 107.5; DB 22; Length Best Local Similarity 26.6%; Pred. No. 0.0083; Matches 38; Conservative 24; Mismatches 62, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
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23-AUG-2000, 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 53254; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                              137
                                                                                                                                      193 FGCLRAGQYPRALELL--LRVLP 213
                                                                                                                                                                                                                                  138 VE----FPRKHLTGNFAEEMIC-EPPPALQEYLGLLYAIRCVERSREFLDFLTRPELREA 192
                                                                                                                                                                                       86 LEEFPAFPRAQVFGRFEASVDSPERRKGAEDLLRFTVHIPALNNS------POLKEF 136
                                                                                                                                                                                                                                                                                       26 YTVSDPPTHPKGYTEYKVTAQFISKKDPEDVKEVVVWKBYSDFPKLHGDLAYTHPNLFPP 85
                                                                                                                                                                                                                                                                                                                                78 FEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED 137
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Perfect score:
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Published_Applications_AA;*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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		Sequence 6, Appli	619,	Sequence 28, Appl	Sequence 2, Appli	Sequence 10617, A	Sequence 11828, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 811, App	Sequence 2, Appli	Sequence 1051, Ap	Sequence 1003, Ap	Sequence 1182, Ap	Sequence 1035, Ap	Sequence 1046, Ap	Sequence 1052, Ap	Sequence 2, Appli	Description

45	44	43	412	41	40	39	38	37	36	3.5	34	33	32	31	30	29	28	27	26	t.)	24	23	13	21	20
76	76	77	77.5	77.5	77.5	77.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	79.5	80	80.5	80.5	81	81	38	82.5	82.5	82.5	83	83
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Sequence 2, Appli	Sequence 3, Appli	Sequence 615, App	12 A	36,	Sequence 33, Appl	7, 7	Sequence 38, Appl	Sequence 35, Appl	Sequence 39, Appl	37,	34,	Sequence 32, Appl	Sequence 30, Appl	Sequence 2, Appli	Sequence 6, Appli	Sequence 321, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 224, App	Sequence 9, Appli	Sequence 13, Appl	Seguence 1620, Ap	٠,	Sequence 15, Appl

# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1046, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1046
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                                                                                                                     Query Match
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                                                                                                 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE. 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al. TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PTZ32
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                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ParentIn Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PTZ32
                                                                                                                                                                                                                 NAME/KEY: SITE LOCATION: (69)
                                                                                                                                                                                   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                            Y Match 6.6%; Score 108.5; DB Local Similarity 25.9%; Pred No 0.0081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 EFPRKHLTGNFAEEMICERRRALQEYLGLLYAIRCVRRSRE----FLDFLT----RPELRE 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match
7.2%; Score 118; DB 9; Length 173;
Local Similarity 32.3%; Pred. Mo. 0.0013;
hes 40; Conservative 22; Mismatches 40; Indels
                   14 GPITQCTARTQQEA-----PATGP-DLPHPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 EIPSKHVR-NWVPKVLEQRRQGLETYLQAV-----ILENEELPKLFLDFLNVRHLPSLPK 124
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                                                                        41; Conservative
                                                                   21; Mismatches
                                                                                                           DB 9; Length 141;
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US-09-764-868-1035
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                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1182
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                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al. TITLE OF THYENTION: Mucleic Acids, Proteins, and Antibodies
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CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PTZ32
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
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LOCATION: (124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 6.0%; Score 99; DB 9;
Local Similarity 33.7%; Pred. No. 0.065;
hes 30; Conservative 12; Mismatches
                                                    95 VYQIIVIQTGSFDNNKAVLEFFYSDFAKLQKALLKTFREEIEDVEFFRKHLTGNFAEEMI 154
                                                                                                       / Match 60%; Score 98 5; DB 9; Length 66; Local Similarity 36.5%; Pred. No. 0.025; ndels 23; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LPPKKLIGNMDREFIAERQKGLQNYLNVI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 TAAIEASQSLQSHTEYIIRVQRGISVENSWQIVRRYSDFDLLNNSL------QIAGLSLP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 SARIEEPKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIE--DVE 139
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7 LYTLTVIGPGPPDCQPAQISPRYSDFERLHRNLQPQFRGPMAAISFPRKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 141
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SEQ ID NO 1003
LENGTH: 165
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                                                                                                                                                             Query Match
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CURRENT APPLICATION NUMBER: US/09/764,868
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1) OTHER INFORMATION: Xas equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
      6.0%; Score 98.5; DB 9; Length 165;
Local Similarity 42.1%; Pred. No. 0.09;
local Similarity 42.1%; Pred. No. 2.09; Indels
local Similarity 42.1%; Pred. No. 2.09; Indels
13 PGSTXAMDPLPAAAVGAAAEÄEADEEADPPASDLPTPQAIEPQAIVQQVPAPSRMQMPQG 72
                                                                                                                                    Local Similarity
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                                                 7 PGSPGCMGPI------TQCTARTQQEAPATGPDLPHPG-------PDG 41
                                                                                                      Conservative 27; Mismatches
                                                                                                                                  23.3%;
                                                                                                                            Score 98; DB 9
Pred. No. 0.21;
                                                                                                                                                     DB 9; Length 278;
                                                                                                         62, Indels
                                                                                                      Gaps
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; Sequence 811, Application US/09764868 ; Patent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510

US-09-764-868-811

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LENGTH: 2930; TYPE: PRT; ORGANISM: Homo sapiens US-09-957-837A-2
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SEQ ID NO 2
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Best Local Similarity 22.7%; Pred. No. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/957,837A CURRENT FILING DATE: 2001-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1711 GQQAESKQSKREMER------EITPSLFSSPVAEIKVNWFKNRDEMLVVLPKLD 1758
1974 ATEMTLORY 1982
                                                                                                   1914 ATVALQYPKAIFQKHRIEQWKTWMEELICNTTVERCQELYRKYEMQYAPQPPPTVCQFIT
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                                                                                                                                                                                                                                                                                                                   1818
                                               306 LKELTVREY 314
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                                                                                                                                                     272 AMVRLAYALG-----KDFVTLQERL-----
                                                                                                                                                                                                                                                         221 HCPAAAVPALC-----AVLICHRDLDRPAEAFAAGERALQRLQAREGHRYYAPLLD 271
                                                                                                                                                                                                                                                                                                                                                                  161 LQEYLGLLYAIRCVRPSPEFLDFLTPPELREAFGCUPAGQYPPALELLLPVLPLQEKITA 220
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                                                                                                                                                                                                                                                                                                             VQEAIQV------KLNEFEQWIT--HYQAAFNNLEATQ----LASLLQEISTQMDLG- 1862
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                                                                APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Tsai, Fong Ying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09784249 Patent No. US20010027184A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mat ches
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LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
TITLE OF INVENTION: 13237, 18480, 2245 OR 16228 NOVEL HUMAN TITLE OF INVENTION: PROTEIN KINASE MOLECULES AND USES THEREFOREILE REPERRENCE: 48155-20020.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURPENT APPLICATION NUMBER: US/09/784,249
CURRENT FILING DATE: 2001 02-15
PRIOR APPLICATION NUMBER: 08/997,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-12-23
PRIOR APPLICATION NUMBER: 60/051,446
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sanjay Kumar
APPLICANT: Cheng Zou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SERINE/7 FILE REFERENCE: GH-70124-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (223)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 496
                                                                                                                                                                                                                                                                                                                                                                                                                         140 FPRKHLTG NFAEEMICERRRALQEYL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 FPRKHLTG-NFAEEMICERRRALQEYL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 5.7%; Score 93.5; DB 10; Length 496; Lenal Similarity 31.0%; Pred No 1 %;
                                                                                                                                                                                                                                                                                                                                                                           72 IPAKRIFGDNFDPDFTKOPRAGINEFI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 IPAKPIFGDNEDPDFIKQPRAGINEFI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match
5 7%; Score 93.5; DB
Local Similarity 31.0%; Pred. No. 0.55;
hos 27; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 IPSSDEHREKKKPFTVYKVLV----SVGRSEWFVFPRYAEFDKLYNTLKKOF--PAMALK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 JASAPIEEPKVSKFVVYQIIVIQTGSEDNNKAVLERPYSDFAKIQKALLKTFPEEIEDVE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 IPSSDEHREKKKPFTVYKVI.V----SVGRSEWFVFRRYAEFDKLYNTLKKOF PAMALK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 IASARIEERKYSKEVYYGIIVIGTGSEDNNKAVLERRYSDFAKLQKALLKTEREEIEDVE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                    SEQ ID NO 11828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Far: L.
APPLICANT: Zyskind, Judith I
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                         Matches
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11828, Application US/09815242 Patent No. US20020061569A1
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PPIOP APPLICATION NIMBEP US 60/210,028
PPIOP FILING DATE: 2000-07-18
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CURRENT FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                        PRIOR AFFLICATION NUMBER, 60/269,308
PRIOR FILING DATE, 2001 02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PAPPLICATION NUMBER: 60/253,625
PRIOR PAPPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000 12-22
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PRIOR FILING DATE: 2000-03-21
PRIOP APPLICATION NIMBER: 60/206,848
PRIOP FILING DATE: 2000-05-23
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1066
                                                                                                                                                                                                                                                                                           LENGTH: 1162
                                                    106 FONNKAVLEPRYSDFAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 FPRKHLTGNEAEEMICEPPRALQEYLGLLYAIPTVPPSPEELDE 183
84 EDHAETTLVGEYAQYAETSIRFRYSRDOQUTYFLHGTFORFRCTTDTFLGTGLGFROTGI 143
                                                                                                                             Match 5.4%; Score 89; DB 10; Length 1162; Local Similarity 23.6%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 FAKGIVFGPFDETVIEEPPQCAEDLLQFSANIPALYNSKQLEDF 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 ERYVSYFVVYQI IVIQTOSELMNEAVLEREYSDEAKLQKALLKTERBEIEDVE---- 139
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Zyskind, Judith W.
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                                                                                                      Conservative
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                                                                                                      Mismatches 80; Indels
                                                  QKALL----KTEREEIEDVEE-----PEKHL- 145
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                                                                                                                                                                                                                                                                     Matches
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CUPPENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 1045
                                                                                                                                                                                     472
    546 ELTEVEKTVQRFTETLSALGAEKQQKE---
                                       153 MICERRRALQEYLGLIYAIRCVRRSREFLDFLTRPEIREAFGCIRAGQYPRALELLLRVL 212
                                                                                                                                106 FDNNKAVLERRYSDFAKLOKALLKTFREEIE------DVEFPRKHLTGNF------AEE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 ARVEQSIQHGQQRQ 314
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                                                                                                                                                                                                                 48 GLSSNSSMTTRELOQYWONQKCPW-KHVKLLFEJASARIEEPKVS-KFVVYOTIVIQTCS 105
                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                      AE--EAKLQTKKSQWASLQIQRLSLLLEEGEPCPVCGSLEHPKQQTHQEVSLEEIDQAER 545
                                                                                                                                                                            GTLEKANFECSSVADHWONFVERWOKNOKAWOKISONOVELHELTORFAVEO----OOKS 487
                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRPEUREAFGCURAGQYPRALELLLRVUPLQEKUTAHCPAAAVPALCAVL--LCHRDLDR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T--DLREELG------ROLERLHROAQSAEKYQEH--KAEERQLKAQIGAVRWRDINE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TGNFAEE-----MICERRALQEYLGLLYAIRCVRRSREFLDFL 184
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                          5.3%;
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                                                                                                                                                                                                                                                                %; Score 88; DB 10; Length 10;
%; Pred. No. 12;
57; Mismatches 128; Indels
--SQLQEQ----EAAYTEEQEQLAAQFA 594
                                                                                                                                                                                                                                                                                                               DB 10; Length 1045;
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; Sequence 28, Application US/10042417; Patent No. US20020123082A1
, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10098979 Patent No. US20020177207A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                           APPLICANT: Pagano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/304,101
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: to be assigned
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sugiyama, Janice
APPLICANT: Cimbora, Daniel
TITLE OF INVENTION: TSG101-INTERACTING PROTEINS
FILE REFERENCE: 1907.06
CURRENT APPLICATION NUMBER: US/10/098,979
CURRENT FILING DATE: 2002-03-14
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2002: NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 LSSNSSMTTRELQQYWQNQK------CRWKHVKLLFE-IASARIEER-KVSK 92
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22.4%; Pred. No. 33;
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SEQ ID NO 28
LENGTH: 621
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ORGANISM: Homo sapiens
10:042 417-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999 CURRENT APPLICATION NUMBER: US/10/042,417 CURRENT FILING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: 45/260,179 PRIOR FILING DATE: 45/260,179 PRIOR FILING DATE: 2001-01-5 NUMBER: GF SEQ ID NOS: 89
                                                                                                           255 IELQSQ···----VLDAMNYVLY 270
                                                                                                                                                                                                              205 YCNPLSDISLKDIQAQID-----SIVELVCKTL---PGINSPHPSLAFKAGESSMIME 254
                                                                                                                                                                                                                                                                  201 YPRAL-ELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDLD--RPAEAFAAGERAL--- 254
                                                                                                                                                                                                                                                                                                                     145 EDELVCILNMEGRKALTWKYYAKKILYYLPQQKILNNLXAFLQQFDDYESYLEGAVYIDQ 204
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                                                                                                                                                                                                                                                                                                                                                                                                                             103 ------ROKAGLEAR-----KIVASFSKRFFSEHVPCNGFSDIENLEGPEIF----F 144
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Result
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Maximum DB seq length: 200000000
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               US-08-906-865-4
US-09-129-669-4
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US-09-413-814-80
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US-09-413-814-80
US-09-625-322-4
US-08-625-322-4
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ADDESSEE David A. Jackson, Esq.  ADDESSEE: 411 Hackensack Ave, Continental Plaza, 4th  STREET: 411 Hackensack  STREET: 400   CITY: Hackensack  STATE: New Jersey  COUNTRY: USA  ZIP: 07601  ZIP: 07601  ZIP: 07601  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: LEM PC comparible  OPERATION SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT AFFLICATION DATA.  APPLICATION HUMBER: US/08/906,865  FILING DATE.  CLASSIFICATION: 536  AITCRNEY/ASNT INFLEMATION:  HAME Jackson Esq. David A  REGISTRATION NUMBER: 26,742  REFERENCE/DOCKET NUMBER: 600-1-202  TELECOMMUNICATION INFORMATION:  TELEPHONE: 201-84-5800  TELEPHONE: 201-84-5800  TELEPHONE: 201-84-5800  TELEPHONE: 201-84-1684  INFORMATION FOR SEG ID NO: 4:  SEQUENCE CHARACTERISTICS:  LENGTH: 696 amino acids  STRANDEDNESS: single  TOPOLOGY: linear  MOLECULE TYPE: protein  DESCRIPTION: /desc = "Synapsin Ia"  PRESCRIPTION: /desc = "Synapsin Ia"  PRESCRIPTION: /desc = "Synapsin Ia"  DESCRIPTION: /desc = "Synapsin Ia"  PRESCRIPTION: /desc = "Synapsin Ia"	RESULT 1  US-08-966-865-4 ; Sequence 4, Application US/08906865 ; Patent No. 6040168 ; Patent No. GOMATION: APPLICANT: Greengard, Paul APPLICANT: Forton, Barbara APPLICANT: Kao, Hung-Teh TITLE OF INVENTION: BNA ENCODING THE HUMAN SYNATERN IN GENE TITLE OF INVENTION: AND USES THEREOF UNMBER OF SEQUENCES: 4	28 78.5 4.8 706 2 US-08-689-276A-4 Sequence 4, Appli 30 78 4.7 3111 2 US-08-460-09-4 Sequence 4, Appli 31 78 4.7 3111 2 US-08-460-09-4 Sequence 4, Appli 32 76.5 4.6 557 4 US-09-271-815-2 Sequence 2, Appli 33 76.5 4.6 2101 1 US-08-466-390-4 Sequence 2, Appli 36 76.5 4.6 2101 1 US-08-467-981-4 Sequence 4, Appli 36 76.5 4.6 2101 1 US-08-467-781-4 Sequence 4, Appli 37 76.5 4.6 2101 1 US-08-477-81-4 Sequence 4, Appli 39 76.5 4.6 2101 1 US-08-477-81-4 Sequence 4, Appli 39 76.5 4.6 2101 1 US-08-487-4 Sequence 4, Appli 39 76.5 4.6 2101 2 US-08-195-487-4 Sequence 4, Appli 39 76.5 4.6 2101 2 US-08-195-487-4 Sequence 4, Appli 39 76.5 4.6 2101 4 US-08-195-487-4 Sequence 1, Appli 40 76 4.6 2101 5 FCT US93-06160-4 Sequence 1, Appli 39 76.5 4.6 2101 5 FCT US93-06160-4 Sequence 5, Appli 39 76.5 4.6 2101 5 FCT US93-06160-4 Sequence 5, Appli 39 76 4.6 454 4 US-09-3764-970-5 Sequence 5, Appli 39 76 4.6 2539 4 US-09-383-3 Sequence 9, Appli 39 76 4.6 2639 4 US-09-383-3 Sequence 9, Appli 39 76 4.6 2639 4 US-09-383-3 Sequence 9, Appli 39 76 4.6 2639 4 US-09-383-3 Sequence 9, Appli 39 76 4.6 2041 1 US-08-419-414-9 Sequence 9, Appli 30 76 4.6 2639 4 US-09-383-3 Sequence 9, Appli 30 76 4.6 2041 1 US-08-419-414-9 Sequence 9, Appli 30 76 4.6 204 1 US-08-419-414-9 Sequence 9, Appli 30 76 75 75 75 75 75 75 75 75 75 75 75 75 75
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Best Local Similarity

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RESULT 3 • US · 09 417 · 822 · 2
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NUMBER OF SEQ ID NOS: 8
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TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
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                                                                                                                                                                                                                                                   165 IGILLYAIRCVRRSREFI.DE-LTRPELREAFGCLRAGQYPRALELLLRVLPLQEKLTAHCR 223
                                                                                                                                                                                                                                                                                                      119 IDEPHTDWAKYEKG--KKTHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVLRN----- 170
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                                                                                                                                                                                                GVKVVPSLKP- DEVLIP - QHAESMARNGDY RSL - VIGLO
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GENERAL INFORMATION:
APPLICANT: Keegan, Kathy
TITLE OF INVENTION: ATR-2
FILE REFERENCE: 27866/3563
CURRENT APPLICATION MIMPEP US/02
CURRENT FILING DATE: 199-10-14
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 2930
                     SEQ ID NO 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93, Application US/09413814
                                                                           CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARWIEF AFFLICATION NUMBER: DE 190 4C 473.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
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APPLICANT: Bristol-Myers Squibb,
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
                                                                                                                                                                                                                        TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or TITLE OF INVENTION. heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                          APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                      SOFTWARE: PatentIn Ver.
LENGTH: 3072
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                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide TITLE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535 CUBRENT APPLICATION NUMBER: US/09/413,814 CUBRENT FILING DATE: 1994-10-07 EARLIER APPLICATION NUMBER: DE 198 46 493.2 EARLIER FILING DATE: 1994-10-09 NUMBER OF SEQ ID NOS: 107 NUMBER OF SEQ ID NOS: 107 NUMBER OF SEQ ID NOS: 107 NUMBER: Datentin Ver. 2.1
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APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
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APPLICANT: Cino, Paul
                                                                                                                                                                                                                                                                                    LENGTH: 3079
TYPE: PRT
ORGANISM: Sorangium cellulosum
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                                                                   896 EHPTLAQLASHLSSGAAS--TSAAAATALERGLTRPD-----GPSSPRVAT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 PYSDFAKLOKALLKTF-PESIEDVEFPRKHLTGNFAEE--MICE------RRRAL 161
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Local Similarity 21.1%; Pred. No. 3.7,
hes 75; Conservative 34; Mismatches 126; Indels 120; Gaps
57 TPELOOYWONOKOPWKHVKLLFEIASARIEERKVSKFVVYQI-IVIQTGSFDNNKAVLER 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 TRELIGEYMONOMORHAMILLEEIASABIBABYVYVYVOI-IVIOTOSEDMUNAVLER 115
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                                                                                                                                                                                              Local
                                                                                                                  EHPG-----SPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMT 56
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                                                                                                                                                                         75;
                                                                                                                                                                                              Similarity
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                                                                                                                                                                       Conservative
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21 1%; Pred Nc 3 7,
tive 34; Mismatches 126; Indels 120; Gaps
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                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949
INFORMATION FOR SEC ID NO. 2
SEQUENCE CHARACTERISTICS.
LENGTH: 522 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gill, Gordon N.
APPLICANT: Kurten, Richard C.
APPLICANT: Cadena, Deborah L.
TITLE OF INVENTICK: Sorting Nexins and Methods of Using Same
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1130 WRKALDG-ATTAIDLPRDFAFHDASPRFGRAHAITLFKFLTGALARLAFERGTTL 1183
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149 FAESMICERFRADQETUGLIYAIHOVEFSFEFLDELIFFFEUS SAFGOLF - AJ
                                   174 PLEPSKOFAVKPPFSDFLGLYEKL----SEKHSONGFTVPPPPEKSLIGMTKVKVGKEDS
                                                                            105 -SFDNNKAVLEPPYSDFAKLQKALLKTFPEETEDVEF----PRKHLTG------N 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 ELLLRVLPLQEKLTAHCPAAAVPALCAVI.ICHPELERPAEAFAAGERALGREGAFFGHFY
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STATE: California
                                                                                                                                                                                                                Match 5.2%, Score 85.5, DB 1, Local Similarity 21 6%; Pred No. 0 76;
                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cat
REGISTRATION NUMBER:
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                                                                                                                  SSKPQPTYEELEEEEQEDQ------FDLTVGITDPEKIGDGMNAYVAYK-VTTQTSL 173
                                                                                                                                                       SSMSSMTTRELLETWENDETORWENDELEEIASAPIEEPKV----SKEVVYQIIVIQIG- 104
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                                                                                                                                                                                                                                                                                                                                    amino acid
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4370 La Jolla Village Drive, Suite 700
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N: 435
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                                                                                                                                                                                                                                  Length 522,
.VE 1.2
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                                                                                                                                                                                                                  Patent No.
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APPLICANT: Hunt, Henry D
APPLICANT: Fulton, Janet
TITLE OF INVENTION: Production of Antisera Specific to Major
TITLE OF INVENTION: Histocompatibility Complex Molecules in (
FILE REFRERENCE: DRt 0064 96 - Larry D. Bacon et al.
CURRENT APPLICATION NUMBER: US/08/890,719A
CURRENT FILING DATE: 1997-07-09
EARLIER APPLICATION NUMBER: 60/021,685
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  TITLE OF INVENTION.
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Local Similarity 24.7%; Pred. No. 0.44;
hes 54; Conservative 24; Mismatches 67, Indels
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                      Sparks, Andrew
                                               Vogelstein, Bert
                                                                 Kinzler, Kenneth
                                                                                               Morin, Patrice
                                                                                                                Clevers, Hans
Korinek, Vladimir
                                                                                                                                                                Barker, Nick
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Beta Catenin, TCF-4, and APC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kagan, Sarah A
PEGISTNATION NUMBER: 32,145
PREFERENCE/INONERT NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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OPERATING SYSTEM: DOS
SOCTWARE, FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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STREET: LVV.
CITY: Washington
TTATE: DC
TTATE: TCA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ADDRESSEE: Banner & Witcoff,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES.
445 RHLHPQVSPLLSA 457
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                                         260 REGHRYYAPLIDA 272
                                                                               400 ----EKAAAPAPFLPMTVLAAPGPQLPRTHPHTICCP-----
                                                                                                                    211 VEPEQEKETAHCPAAAVPAECA------VELCHPDEBEAEAFANGERAEGE 259
                                                                                                                                                                                                                                             316 KVÍAECTLKESAÁINQILGPRWHALGE:
                                                                                                                                                                                                                                                                                                                               268 PPSG--KQELQFFBRNLKTQ------
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TELEPHONE: 202-508
9299
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THE GEAX. 202-508
                                                                                                                                                                                                                                                                                      99 IVIQTGSFDNNKA---VLEPRYSDFAKLQKALLKTFPEEIEDVEFPPKHLTGNFAEEMIC 155
                                                                                                                                                                                                                                                                                                                                                                      51 SNSSMTTRELQQYWQNQKCPWKHVKLLFEIASAPIE-----ERKVSKEVVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PEHPGSPGCMGPITQCTARTQQEAPATGPDLPHP-----GPDGH--LDTHSGLS 50
                                                                                                                                                               ERQLHMQLYPG--WSAPTNYGKKKRESEEKHQESTTGGKKNAF
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                                                                               -ASPQNCLLALRS 444
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; Sequence 8, Application US/09003687A ; Patent No. 5998600 ; GENERAL INFORMATION:

APPLICANT:

Barker, Nick

US-09-003-687A-8

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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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TITLE OF INVENTION: Beta Catenin, TCF-4, and A
TITLE OF INVENTION: Interact to Prevent Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                               268 PPSG--KQELQPFDRNLKTQ------AESKAEKEAKKPTIKKPLNAFMLYMKEMRA 315
445 RHLHPQVSPLLSA 457
                                   260 REGHRYYAPLLDA 272
                                                                                                   211 VLPLQEKLTAHCPAAAVPALCA------VLLCHPDLDPPAEAFAAGEPALQPLQA 259
                                                                                                                                                                                                           116 KVIAECTIKESAAINQILGPPWHALSP-----EEQAKYYELARK----
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                 51 SNSSMTTPELQQYWQNQKCPWKHVKLLFEIASARIE-----ERKVSKFVVY----QI 98
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                                                                                                                                     EPQLHMQLYPG--WSAPDNYGKKKPPSPEKHQESTTGGKPNAF-----GTYP-----
                                                                                                                                                                       ERRRALQEYIGILYAIR-----CVRRSREFLDFLTRPELREAFGCLRAGQYPRALELLLR 210
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                                                                   ----EKAAAPAPFLPMTVLAAPGPQLPRTHPHTICCP-----
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97430 BMB UT
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1001 G Street, N.W.
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Korinek, Vladimir
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E: No. 5998600e
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22.0%; Fred. No. 1;
ative 35; Mismatches 95; Indels 114, Gaps
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                                                                   -ASPQNCLLALRS 444
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; Patent No. 5804412
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Best Local Similarity 22.0%, Pred. No. 1;
Matches 69; Conservative 35, Mismatche
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                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gill, Gordon N.
APPLICANT: Kurten, Richard C.
APPLICANT: Cadena, Deborah L.
TITLE OF INVENTION: Sorting N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1998-08-20
EARLIER APPLICATION NUMBER: 08/821,355
EARLIER FILING DATE: 1997-03-20
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EARLIER FILING DATE: 1998-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to TITLE OF INVENTION: Prevent Cancer FILE REFERENCE: 1107.75741 CURRENT APPLICATION NUMBER: US/09/136,605A
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APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
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COMPUTER READABLE FORM:
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                        21P:
                                                                   CITY: San Diego
STATE: California
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                                                COUNTRY:
                                                                                                                        STREET:
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                                                                                                                                                   ADDRESSEE:
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                          92121
                                                                                                                      E: Campbell and Flores
4370 La Jolla Village Drive,
                                                   USA
                                                                                                                                                                                                                         Sorting Nexins and Methods of Using Same
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                  S-08-622-353-7
Sequence 7, Application US/08622353
Patent No. 5700925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                    (RNERAL INFORMATION:
APPLICANT: Bishai, William R
APPLICANT: Young, Douglas B.
APPLICANT: Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 9-UD 1955
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         APPLICANT: Demaio, James
TITLE OF INVENTION: A STATIONARY PHASE, STRESS RESPONSE
TITLE OF INVENTION: SIGMA FACTOR FROM MYCCHACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 TLLQDPDLRQ---FLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWFE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 HVV1FVATSSRKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYL....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 QI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 ERÇÖÇFENLIYÇELKELHVSVEA - --- LVCHRKELSANTAAFAKSAAMLGNSEDHTÁL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 DELTEPELREAFGCLRACOYPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
4.9%; Score 81.5; DB 1; Length 451;
Local Similarity 19.9%; Pred. No. 1.7;
hes 60; Conservative 45; Mismatches 96, Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
                                                             COUNTRY:
                                                                                     STATE:
                                                                                                                          STREET:
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                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 LFEIASARIEERKY----SKFVVYQIIVIQTGSFONNKAVLERPYSDFAKIQKALLKTFP 132
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                                                                              Washington DC
                                                                                                                     1001 G Street, eleventh floor
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Floppy disk
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RESULT 13
US:08 622 352A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.3%; Soure 81, DB 1, Length 287;
Best Local Similarity 21.2%; Pred. No. 0.97;
Watches 66, Conservative 38, Mismatches 108, Indels 109,
                                                                                                                                                                                                                       GENERAL INFORMATION.

APPLICANT: Bishai, Willia

APPLICANT: DeMaio, James

TITLE OF INVENTION FROM

TITLE OF INVENTION. FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWAPE: Patentin Polease #1 0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 GLILDRIGYED------PALDGVE--HRDLVR
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THI TERAX: 202-508-9299
                                                ZIP:
                                                                   COUNTRY:
                                                                                            STATE:
                                                                                                            CITY: Washington
                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/622,353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SPEHPGSFGCMGF1TQCTARTQQEAFATGPDLFHFGFDGHLDTHS------GLSSN 52
                                                20005-3918
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                                                                                                                                   E: Pillsbury Madison & Sutro, L.L P 1100 New York Avenue, N.W.
                                                                     USA
                                                                                                                                                                                                                                                                                          Bishai, William R.
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US-08-826-390-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08826390
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bishai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                          APPLICANT: DeMaio, James
APPLICANT: DeMaio, James
APPLICANT: DeMaio, James
TITLE OF INVENTION: Stationary Phase, Stress Response
TITLE OF INVENTION: Sigma Factor From Mycobacterium tuberculosis, and
TITLE OF INVENTION: Regulation Thereof
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                    COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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LENGTH: 287 amino acid
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 FONNKAVLERPYSOFA--KLOKALLKTEREEIEDVEEPRK-----------------HLTGNFA 150
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                                                                                                                                                                                        STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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                                                                                                                                               COUNTRY:
                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 SSMTTPELOOYWONOKCPWKHVKL---LFEIASARIEERKVSKFVVYOI--- IVIOTGS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Match 4.9%; Score 81; DB 2, Length 287, Local Similarity 21.2%; Pred. No. 0.97; Local Similarity 38; Mismatches 108; Indels 100; Gaps
                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 APQAPPAP-----PAQAQAQAQAPAQAQEAPAPQRSRGADTRALTQVLFGELKGLAPG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE----MICERPRALOEYIGLLYAIPOVPREREFLDFLTRPELREAFGCLRAGQYFRALE 206
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                                                                                                                                                 USA
                      Word Perfect
                                                                                                                                                                                                                                                                                                                                                                                                          Young, Douglas B
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishai, William R.
                                                                                                                                                                                                                                                                                                                                                                                        Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor
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US-08-533-306A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/08533306A
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 66; Conservative 38; Mismatches 108; Indels 100; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-MAR-1996 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for D
TITLE OF INVENTION: Rearrangement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: p:
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-MAR-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/622,353
                                                                                ZIP: 48303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 FDPERGV---QFPTFAMPTVVGEIKFYFFDNVFTVHVPFFLHELWVQVNSATEDLTTAFG 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 LRYYSNLTQSQI 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 LLERVLEIQEKLTAHCEAAAVEALCAVLLCHEDIDEFFAEAFAAGEFALQFIQAFEGH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 EE----MICERFRAUQEYLGINYATROVPRSREETURUTPPELREARGOLFAGGYPRALE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 FDMNKAVLERFYSDFA - KLQYALLFTFEEEIEDVEFFRK
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    STREET: P.O. L. CITY: Bloomfield Hills
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                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                     Markers for Detection of Chromosome 16
                                                                                                                                                                                                                                                                                   Rearrangements
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Search completed: April 20, 2003, 14:08:21 dob time : 21 secs
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TELEPAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2115-00869COB TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    177
                                                                                            622 ELEEEQ 627
                                                                                                                                                                                                                                  234 LLCHRULDRPAEAFAAGERALQ----RLQAREGHRYYAPLLDAMVKLAYALGKDFVTLQE 289
                                                                                                                                                                                                                                                                               533 KDFORELED- ARASEDELFATAKENE-KKAKSLEADLMOLOEDL----AAAERARKOA 584
                                                                                                                                                                                                                                                                                                                                                                         473 ORQLHEYETELEDERNERALAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQM 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 RALETOMBEMKTQLEBLEDELQASEDAKLBLEVNMQALKGQFEPDLQAPDBQNEEYRPQL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 FA-KLOKALLKTFREEIED ....-VEFPRKHLTGNFAEEMIC-----ERRRAL 161
                                                                                                                                         290 RLEESO 295
                                                                                                                                                                                     585 DIEKERLAEELASSISCHNALODEKRRIEAR
                                                                                                                                                                                                                                                                                                                                                                                                                        162 QEYL-- --- 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 REQUEEDDELVVD- ------EDNOPQEVSNIEKKOPKFDQELAEEKNISSKYADEPDRA 352
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Local Similarity 21.9%; Pred. No. 4.9;
hos 80; Conservative 31; Mismatches 123; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 RTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQK-------68
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                                                                                                                                                                                                                                                                                                                       SREFIDELTREELREAFGCIRAGGYERALELLLEVIEUGEKLTAHCEAAAVEALCAV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPWKHVKLLF ---- EIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSD 119
                                                                                                                                                                                     IAQLEE 621
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